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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Resi	sult		Query				3
-	Ю	Score	Match	Length	DB	ID	100
		9.4	00	94		F20770	20770
υ	7	26.	87.	30405		0482	004829 Staphyl
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	ഗ	69.	"	38		52046	520460 Seguenc
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υ	12			8682			56 Pla
	13	σ		805		AX599046	346 Seg
	14	7		25865		3	332
	ı,			805		AX598900	300 Seq
U	16	85.2		28620		AC117140	.40 Rattus
C	7	α		84		CNS0180K	375 Botryt
) U	00	4		200		AX457067	167 Sequen
Ç	6	4		25002		AE014820	320 Plasmo
)	20	84.2		25947		HUAC004605	in
	21	m		17554		2	342 Rattus
U	22	œ		13741			s omoH 990
,	23	2		109			761 Drosop
	24	N		16904			328 Zebraf
	25	82.4		34860			521 Wigg
υ	56	4		34998			555 Seguen
υ	27	ď		19687			395 Rattus
υ	28	w		623			193 Sec
υ	29	82		23387		S	798
	30	ä		34975		щ	176 Pla
	31	81.4		15606		115	153 Plasmo
	32	i.		25070		4	348 Plas
	33	H		34705		293	351 Plas
υ	34	H		0066		75	756
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## ALIGNMENTS

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		947 bp DNA	tative t	te cds.						cillales		Ü,	l, a modu	
			Staphylococcus aureus putative transposase gene, partial cds; and	Sark (sark) gene, complete cds.		AF207701.1 GI:11493941		cus aureus	cus aureus	Bacteria; Firmicutes; Bacillales; Staphylococcus.	to 947)	Cheung, A.L. and Manna, A.C.	ation of sar	cus aureus
		AF207701	Staphylococ	Sark (sark)	AF207701	AF207701.1		Staphylococcus aureus	Staphylococcus aureus	Bacteria; F	1 (bases 1 to 947)	Cheung, A.L.	Characteriz	Staphylococcus aureus
RESULT 1	AF207701	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	

840

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721 CAAGGTACACTAGTCTTTTTTTTTTTTTTTTTTTTAGAAATCAAGTTTACGATCATAA 780
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Director-General, Biotechnology Center, Aoki, K., Oguchi, A.,
Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramatsu, K. and
Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (06-MAR-2002) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center; Zchome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
                      541 TACATTAAAAATTAAATCAAGGTTAATTGCGTTTAATAACATTGAACGATAACAATTTAT
                                                                                                                                                                                                                 AGATGCTTTAATTAAAGCTTAAAAGCTACCAACCCATATTTCAGCTTATTAAGCTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguchi, A., Nagal, Y., Iwama, N., Asano, K., Naimi, T., Kuroda, H., Cui, L., Yamamoto, K., and Hiramatsu, K.
Genome and virulence determinants of high virulence
                                                                                                           541 TACATTAAAATTAAATCAAGGTTAATTGCGTTTAATAACATTGAACGATAACAATTTAT
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Staphylococcus aureus subsp. aureus MW2
Bacteria, Firmicutes; Bacillales; Staphylococcus.
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Lancet 359 (9320), 1819-1827 (2002)
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Unpublished

2 (bases 1 to 947)

Cheung, A.L. and Manna, A.C.
Cheung, Ch.L. and Manna, A.C.
Direct Submission
Submitted (22-NOV-1999) Microbiology, Dartmouth Medical School,
College St., Varil 206, Hanover, NH 03755, USA
Location/Qualifiers
Location/Qualifiers
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QOMDLEMENT (5125. .5409)
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COMPLEMENT (2519. . 2734)
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         hypothetical protein, similar to acetyltransferase.
[Genomic island nu Sa 4mw]"
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Whole genome sequencing of meticillin-resistant Staphylococus
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Director-General, Biotechnology Center, Aoki, K. and Kikuchi, H.
Bosyama, A., Nagai, Y., Kuroda, M., Hiramatsu, K. and Kikuchi, H.
Direct Submission
Submitted (30-JAN-2001) Director-General, Biotechnology Center,
National Institute of Technology and Evaluation, Biotechnology
Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bioGenite.go.jp, UKL:http://www.bio.nite.go.jp/,
Tel:81-3-3481-1933, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701842.
                                                                                                                                                                                                                 AP003136 307750 bp DNA linear BCT 11-JAN
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Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College
of Medical Technology and Nursing, Department of Medical
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(E-mail:tohta@sakuta.cc.tsukuba.ac.jp, Tel:81-298-53-3454,
Fax:81-298-53-3454)
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AUTHORS
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Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.
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AP003364 BA000017
AP003364.2 GI:14247707
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Staphylococcus aureus subsp. aureus Mu50
Bacteria, Firmicutes; Bacillales; Staphylococcus.
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338729 CAGAGTICAAACCTIACTATTIAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATIGT 338670
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Pred. No. 2.9e-109;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SAV1945"
complement (8388. .9119)
/gene="SAV1945"
/note="Bacteriophage phiN315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SAV1946"
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                                  complement (7682. .8173)
/gene="sak"
/note="Bacteriophage phiN315
                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (8388. .9119)
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/gene="SAV1946"
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Best Local Similarity 98.4%;
Matches 854; Conservative (
                                                                                                                                     SAV1944"
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418e="truncated-hlb"
/note="SAV1939"
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codon start=1
transl_table=11
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/note="Bacteriophage phiN315"
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/note="Bacteriophage phiN315
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complement (5834. .6184)
/gene="SAV1942"
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	RESULT 6 AE016750, LOCUS LOCUS Staphylococcus epidermidis ATCC 12228, section 7 of 9 of the complete genome. ACCESSION AE016750 AE015929 KENSION AE016750.1 G1:27316220 KEYWORDS SUBMYLOCOCCUS epidermidis ATCC 12228 SOUNCE ORGANISM Staphylococcus epidermidis ATCC 12228 AUTHORS 1 (bases 1 to 30069) AUTHORS Zhang, Y. Ren, S. Li, H., Fu, G., Lu, L., Lu, G., Jia, J., Tu, Y., TITLE Direct Submission	JOURNAL Submitted (65-NOV-2002) Chinese National Human Gencer at Shanghai, 250 Bi Bo Road, Shanghai 201203, China FEATURES 1. 30698 1. 306	trnA	at 0
Oy 500 AAAAGCAAATATTCAAAACTGATTTCAGAATTAGAAGATTAAAATTAAAATTAAATCA 559  Db 338609 AAAAGCAAATATTTCAAAACTGATTTCAGAATTAGAAGAAGGAATTAAAAATTAAATCA 33850  Qy 560 AGGTTAATTGCGTTTAATAACATTGAACGATAACAATTATTAATAAATTATTTAT	Qy         740 TATTITAATATITICTIAGAAAATCAAGITIACGATCATAAATATITICTGCGATATAGC 799           Db         338369 TATTITAATATITICTTAGAAAATCAAGITIACGATCATAAATTITCTGCGATATAGC 338310           Qy         800 TITGGATGGTTCCAAGTATITCTCTATAATTIGTGTGCGATAAGCAAAATTCTAACTG 859           Db         338309 TITGGATGGTTCCAAGTATTTCTCTATAATTTGTGTGCGATAAGCAAAATTGTAACTG 338250           Qy         860 CAAAACCATGTGTAGGCAATTGAGAAATAGCAACACGACAATCGGATGTATTGCTATAAG 919           Db         338249 CAAAGCCATGTGTAGGCAATTGAGAAATAGCAACAGGACAATCGAATGTATTGCTATAAG 338190           Qy         920 AACTAATGGTTTCATAAACTGAATCGAT         947           Db         338189 AACTAATGGTTTCATAAACTGAATCGAT         338162	RESULT 5  AX620460  LOCUS  LOCUS  LOCUS  BEFINITION Sequence 3423 from Patent W002094868.  ACCESSION AX620460  AX620460.1 GI:28449549  KEVWORDS  SCURCE  ORGANISM  REFERENCE  Bacteria; Firmicutes; Bacillales; Staphylococcus.  REFERENCE  AUTHOR  ASTAPHORS  Masignani, V.C., Mora, M.C. and Scarselli, M.C.  TITLE  AUTHORS  TABALOREL: WO 02094888-A 3423 28-NOV-2002;  FEATURES  Chiron Spa (II)  Location/Qualifiers	167 e tch al Similari 382; Cons	DATCAGAAGGACTGGTTTAATAATGAGTAAATTAATGATAT 22  CATCAG-AGGAGTGGTTTAATAATGAGTAAAATTAATGACAT 59  AACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAGA 28  AACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAAGA 28  AACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAAAA

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Patent: WO 02077272-A 386 03-OCT-2002;

Epigenomics AG (DE)
    714 AIGTGTAGGCAATTGAGAAATAGCAACACGACAATGGATGTATTGCTATAAGAACTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic DNA (Homo sapiens)"
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1. 8056
/ organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texon:32530"
/note="chemically treated genomic
a 0 c 371 g 3974 t
                                                                                                                                                             DNA
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Sequence 386 from Patent WO02077272.
AX599046.1 GI:28399186
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                                                                    654 GGTTTCATAAACTGAATCGAT 634
                                                    927 GGTTTCATAAACTGAATCGAT
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                                                                                         97851 AATATTGAATTCTTATACTTATTTTAAATGTACCTTGTAACATGGGGGGGAGAA-T 97793
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                                                                                                                        TTTCGATTTAATACATTAAATGTGAACCTTGCTACAACAAGATGTGCATCAGAAGGAGTG
                                                             80 ATTACCGAATITITATACTTATITGTTTAGAATGAACTTTATAACATAGTTGGATAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGAGAAAAAATAAAATTGATTTAGAATTAGAAAACTATATCAAATAATA 97379
                                                                                                                                                                                                                                                                                                           TAAATCATATTTTAAGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCT
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ch 32.4%; Score 307; DB 1; Length 300698; Il Similarity 80.6%; Pred. No. 1.6e-35; Sonservative 0; Mismatches 90; Indels 2;
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/organism="Staphylococcus aureus"
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/db_xref="taxon:1280"
a _133 c _126 g 279 t
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Pred. No. 2.2e-19;
0; Mismatches 1;
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Sequence 3379 from Patent WO02094868.
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Matches 200; Conservative 0
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Barstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brydon, C., Carters, P., Carter, P., Carderon, E., Charder, C., Carderas, V., Carter, M., Chen, W., Chen, W., Chen, W., Chen, C., Charderon, E., Chardero, J., Chardero, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Dasson, S., Derman, C., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Garta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, E., Hanglai, A., Garta, R., Garra, M., Gunaratne, P., Hanglai, A., Garta, R., Garcia, A., Garra, M., Gunaratne, P., Hanslak, P., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Hines, S., Hladun, S.L., Hodgson, M., Hernandez, J., Hines, S., Hladun, S.L., Hodgson, M., Hernandez, J., Lorensuhewa, L., Lacob, L., Lebow, H., Levan, J., Lawis, L., Li, Z., Liu, J., Li, M., Liu, W., Liu, Y., London, P., Longan, E., Mandartne, R., Martine, R., Martine, M., Martine, M., Matud, P., Martin, K., Martine, R., Martine, S., Municatne, P., Martine, P., Martine, S., Municatne, P., Pals, S., Parks, K., Pals, S., Pals, S., Municatne, P., Pals, S., Pals, S., Municatne, P.,
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*** SEQUENCING IN PROGRESS ***,
586 ACGATAACAATITAATAACGAAGTTATTTATTCAGCATTGGGACATAAAATTAACTTA 645
                                                                                                                                                                                                                                                         646 AAATITAAATATIGAAGATGCTTTAATTAAAGTTAAAGACCAGCCATACCTTATTTCAGC 705
                                                                                                                                                                                                                                                                                                                          TTATTAAGCTTGACACAAGGTACACTAGTCTTTTTATTTTTAATATTTTCTTAGAAAATCA 765
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Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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AC125567.5 GI:24817949
HTG; HTGS_PHASE1; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-9H22,
4 unordered pieces.
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Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

CE 3 (bases 1 to 170627)

S at Genome Sequencing Consortium.

S Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (09-MOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23096537.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome contige scaffold.

(http://www.hgsc.bom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence cands. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shataman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, T., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Taylor, T., Thomas, N., Thomas, N., Tromas, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Valas, R., Willson, W., Waldron, L., Walker, B., Wang, J., Wang, G., Warren, S., Warren, R., Wei, X., White, F., Wailson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Wilson, R., Waldron, H., Worley, K., Wright, D., Wright, R., Wu, Y., Yakub, S., Yen, J., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A. Smith, D.R., Smith, R.A., Smith, H.O., Direct Submission
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TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GDDV
Center project name: GDDV
Center clone name: GDDV
Center name: GDDV
Center
------ Genome Center
Center: Baylor College of Medicine
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

contig of 109158 bp in length gap of unknown length contig of 1022 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length 109158: 0 110280: 0 110380: 0 111540: 0 109159 109259 110281 110381

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                                                                                                                                                                                                                                                                       440
                                                                                                                                                                                                                                                  TACCGAATTITIATACTTATTIGTTTAGAATGAACTTTATAACATAGTTGGATAGAGTTT 141
                                                                                                                                                                                                                                                                                                201
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                                                                                                                                                                                                                                                                                             TCGATTTAATACATTAAATGTGAACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGT
                                                                                                                                                                                                                                                                                                                                          TTAATAATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAG
                                                                                                                                                                                                                                                                                                                                                                                     AAGTITITICAGAGATACAAAAAAGAAGTITCAATTIGAACTATGAAGAAATTIATATATTITA
                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCATATTTTAAGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 -GAGTICAAACCITACTATITAACTAAAGCTITACAAAAGCTAAAAGATITAAAATTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 ATCAAAGAAAGAAGTTTACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 AAAAGCAAATATTCAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAA
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                                                                                                                                                                                                                             ..
..
                                                                                                                                                                                                     Length 170627;
                                                                                                                                                                     4732 others
170627: contig of 58987 bp in length.
                                                                                                                                                                                                                Similarity 48.2%; Pred. No. 6.1e-05;
                                                                                                                                                                                                     8; DB 2;
6.1e-05;
                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-9H22"
                                                                                                                                                          end_sequence:BH341988"
. 30081 c 30017 g 54086 t
                                                                                                                                                                                                     9.8%; Score 92.8;
                                                                           1. .1284
/note="wgs_end_extension
clone_end:Sp6"
                                                                                                           3636. ...4924
/note="clone boundary
clone_end:Sp6
       Location/Qualifiers
                                                                                                                                            site: EcoRI
                                                                                                                                                                                                                           291; Conservative
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INV 29-JAN-2003

linear

Plasmodium falciparum DNA from MAL1P3. AL031746 AL044501 AL031746.9 GI:6594243 ·

PFMALIP3 LOCUS DEFINITION ACCESSION VERSION

RESULT 10

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Mungall, K., Bowman, S., Atkin, R., Baker, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davis, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Larke, N., Lawson, E., Humphray, S., Jagels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortcov, B., Kyes, S., Larke, N., Lawson, D., Lane, A., Maddison, M., McLean, J., Mooney, P., Moule, S., Murphy, J., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-55P-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
On Dec 16, 1999 this sequence version replaced gi:5763807.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.wk/Projects/P_falciparum.
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force="Originally annotated as Plasmodium falciparum,
conserved hypothetical protein but pfam match and other
evidences suggest that it is a putative deoxyribonuclease,
earlier start site possible to make a 412 as protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MENRSKTISQNTIKAHVEANDECKEKKEKYLKCFNNWYKNNFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2848
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complement(join(1392. .1461,1752. .2598,2748. .2848)
                           Plasmodium falciparum 3D7
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy, L., Pain, A., Berriman, M., Bowman, S., Churcher, C., Ha
Bartis, D., Lawson, D., Quail, M., Rajandream, M., Hall, N. and
Barrell, B
Direct Submission
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protein id="CAD49075.1"
db_xref="GI:23477009"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Plasmodium falciparum 3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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falciparum 3D7
falciparum 3D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MA11P3.02"
/gene="MA11P3.02"
/note="contains possible signal sequence. Signal peptide
predicted Signal 2.0 HMM (Signal peptide probabilty
0.640, signal anchor probability 0.357) with cleavage site
probability 0.504 between residues 27 and 28. ScanRegExp
hit to PS00867, Carbamoyl-phosphate synthase subdomain
Pfam match to entry PF01026 TatD DNase, TatD related DNase, score 117.30, E-value 2.96-31
Similar to Plasmodium falciparum conserved hypothetical protein, upf0006 family mallp3.01 SWALL:09U0N6
[EMBL:AL031746) (412 aa) fasta scores: E(): 3.7e-150, 100% id in 412 aa, and to Saccharcmyces cerevisiae putative decxyribonuclease pt1055c yp1055c or yb10512 or yb10511 SWALL:RBFS YEAST (SWALL:P34220) (418 aa) fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMED: 0900N4"
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YISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
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DYIINFIKSTKKMEKDSLNERRSLPNVNIYNIMFSDVPSVTFFVTSCINLENVEVKIF
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NNNVDKIIITCTCLAEIDKSLKICETYDPGGKPLYLSAGVHPTNCYEFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNLNEILLEKNLDIIPGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEKDKEYLENLKNKIIKŶPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIPQLKLVQMFN
LEMPLAMROSETFFKIVLYKELFEKNGWYLHSFDKEDIUHIVQNYKNLYIGVNG
CSIKSLENINAVKKIPLNLLLETDAPWCGYKKTHASYEYIKUTYBKRAYTNLKKIKN
IIKCDDNTIFKERNEPYNIADIAEITYKVREEAVPFDLFCKK"
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/note="Putative ABC transporter

/note="Putative ABC transporter,

Pfam match to entry PP00005 ABC tran, ABC transporter,

score 45.00, E-value 1.7e-09, HMMSmart hit to SM00382,

ATPases associated with a variety of cellular activities,

ScanRegExp hit to PS00211, ABC transporters family
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Similar to Schizosaccharomyces pombe ATP-binding cassette
transporter abc1 abc1 or spac9e9.12C SWALL:ABC1_SCHPO
(SWALL:Q92337) (1427 aa) fasta scores: E(): 4.2e-08,
21.46$ id in 1146 aa"
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/note="Putative centromere"
14884. .20352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="synonym: PFA0585w"
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gene="MAL1P3.02"
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gene CDS gene

CDS

METRY PERTUNDANTAL MANDALALA VELATE CANDALATARIA MANDALATARA TANDALATARA TANDA to vivax A-type 5.8S ribosomal percent id: 88.00 none" ю ., 169 8568 arranaharraharaharaharaharahahahaharahaharahaharahaharah TCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTAAGAAGTGAGTCTAACG 349 50 AAAATAAAAAATATCAATAAGTTGGAGTCATTACCGAATTTTATACTTATTGTTAG 110 AATGAACTTTATAACATAGATAGAGTTTTCGATTTAATACATTAAATGTGAACCTT /product="18s ribosomal RNA A-type" /note="18s rRNA exppressed in asexual stage parasites" /product="ITS1 A-type" /note="ribosomal operon internal transcribed spacer 1 expressed in asexual stage parasites" 26439. .26559 170 GCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGATATA Gaps during asexual development' /product="ITS2 A-type" /note="ribosomal operon internal transcribed spacer expressed in asexual stage parasites" 27436. .31539 gene="mall\_5.8srNA" /product="5.8S ribosomal RNA" /note="5.8S ribosomal exppressed in asexual stage Indels 13; 9.7%; Score 91.4; DB 3; Length 67970; 47.6%; Pred. No. 0.00013; tive 0; Mismatches 396; Indels 13; /note="28s rRNA expressed during asexual deve complement(join(31966. .32476,32675. .32775)) /gene="WAL1P3.04" /note="synonym: PFA0610c" complement(join(31966. .32476,32675. .32775)) /gene="MAL1P3.04" LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD" RNA (A-type)" product="28s ribosomal 26439. .26559 /gene="mall 5.8srNA" 26439. .26559 23896. .26044 26560. .27435 parasites Conservative Similarity

g 8 Db ò g  $\stackrel{>}{\circ}$ Db ò g  $\dot{\circ}$ g ò οg ò g ò g

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/protecin_id=+AAO10414.1"
/db_xref="GI:27544844"."
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DPMGGGDPILYQHLFWFFGHPEVYILLLPGFGLISQIIMNESGKKEIFGNLSMIYAML
GIGFLGFIVWAHFMFTVGLDIDTRAYFTSATMIIAIPTGIKVFSWLATYHGSKLNFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFMWSIGFILMFTIGGLTGIMLSNSSIDIILHDSYYVVGHFHYVLSMGAVFSITASFI
HWFPLISGLMMNQKWLKFQFFFMFIGVNLTPFPQHFIGLMGMPRRYSDYPDSYYCWNM
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complement(1446. .1512)
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3957. .4124
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       product="tRNA-Met"
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/note="cox1"
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/gene="ND2"
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Melipona bicolor
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
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(Dases 1 to 14422)
Silvestre, D. and Arias, M.C.
The mitochondrial genome of Melipona bicolor (Apidae, Meliponini)
                                 350 AAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAACTAAAG
                                                                                                                                                                                   470 GAACAGITATTGTTTATGTTACAGATACACAAAAGCAAAT-----ATTCAAAAC
                                                                                                            410 CTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAAGAAGTTTACAAGACGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  다.
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Silvestre, D. and Arias, M.C.
Direct Submission
Submitted (0.JAN-2002) Biologia, Instituto de Biociencias,
Matao, 277, Sao Paulo, SP 05422970, Brazil
Location/Qualifiers
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Melipona bicolor mitochondrial genome, partial sequence.
AF466146

    11. 14422
/organism="Melipona bicolor"

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194. .262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 90.6; DB 3; Length 14422;
Pred. No. 0.00028;
0; Mismatches 379; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transT_table=5
/product="NADH dehydrogenase subunit 4L"
                                                                                            subunit
                                                                   /transl_table=5
/product="NADH_dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                            complement (9377, .9655)
/gene="ND4L"
complement (8044. .9366)
                                          /codon_start=1
/transl_table=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon start=1
                                                                                                                                                                                                                                                                                                                                                                             /gene="ND4L"
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Best Local Similarity 47.2%;
Matches 345; Conservative
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IMFSLAMLCGFPLVGFYSKOLMIETYYMKKMSIFCLMILIFSTVLTISYSRRIMKNL
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| S666. .6019
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                                                                                                                                                                                                                                                                                                                                                                                                         note="cox3"
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FYDHINS SENR CS FKOLKKOOT DDNYKH I IMCKEKY PPANK DHEKKNINT CGNIN I BK
BOKKOLLKA Y FLKGNKLDDIO LOLLSELY YM YMRLLE BEOSLKILS IKKNIHLLEKKME
FDKDNKI I YLINS AD YWNYDEN I KRESKNEEREN IN SEAS FPFLLSKWI I HLEKKME
FDKDNKI I YLINS AD YWNYDEN I KRESKNEEREN IN SEAS FPFLLSKWI I HLEKKME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKIKDTYNDDDDYDYEKEEDLYIQKNIDDYIYOYNTIGMKSLEEFKNQFIEQADIEPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Signal peptide predicted by SignalP 2.0 HMM (Signal peptide probability 0.635, signal anchor probability 0.287) with cleavage site probability 0.594 between residues 21 and 22; CDS conserved in p. knowlesi and P.yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INEQYPIIKNEKTVLDILNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /KNKI KKYLTYLINNNI SNDLYPYNI SYNKI YNQNKYKNRKNFSHI FYSLKNDIHLLLF
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Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
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Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Horneby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Salandrem, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Barrell, B.G.
664 AATAAATTATTCATGAATGAAATGGGAATATTCTTAATTTTAAAAATATTTAATAAAA 605
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ON Oct 2, 2002 this sequence version replaced gi:7711064.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum MAL3P5, complete sequence.
AL034456 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179 AL844502
AL034556.4 GI:23477013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete nucleotide seguence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum 3D7
plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 86826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; centromere; CTRP protein; initiation factor B4;
Serine/threonine protein phosphatase.
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                                                                                777 ATABATATTT 787
                                                                                                                                                                      604 AAAATTTATT 594
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10448855
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PFMAL3P5/c
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PUBMED
REFERENCE
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Complement(join[13653. .1754,18005. .19353))

/note="MAL3F5.4"
/note="synonym" PFC0590c"

complement(join[13653. .1754,18005. .19353))

/note="sylonym" PFC0590c"
/note="sylonym Peptide predicted by SignalP 2.0 HWM (Signal peptide probabilty 0.921, signal anchor probability 0.075)

with cleavage site probability 0.888 between residues 20 and 2. revised: changed donor in comparison with P. knowlesi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIDYIENNIIYSYIKSFRATPPITKIYLGAFLLSVLIHMNKNYYKLILPDFNKIFK
REBUKALPPYLYIGNIYLQYILAMPKINIYMSKSTREISHYKENDELITETTSYISHLL
PTIMAMNYNENIAMPKLYIHNEYQYILAMPKINIYMSKSTISHSKSTRINSSNNN
HYNNSKNIDIKKEQYNHLGYVESTYILYYWSRINBGTLINCFELFFIKAEVPFFII
ONLLLYNBESIKPASFIRSSYLEFTSKYFKENYKRILAKTLLKYNHTYPELDYRKEE
KNGPLPPLQKCYIHNYPRINTWKHMISDLRKNIEDFORTLLKYNHTYPELDYRKEE
KNGPLPPLQKCYIHNYPRINTWKHMISDLRKNIEDFORTLKYNTYNTIILLK
LPNKEIKNYVDFMIILKLLSKYIKIEKKYLLYICEQIBHEIYKFRTDLLLLLLRK
KFENHLNNYNINLSKSILMWRNKNIKYSKOLALIILSKYNKEIPPRSIL
KNETHLNNYNINLSKSILMWRNKNIKYSKOLALIILSKYNKEIPPRSIL
YNSTDLMFLYIGSLHTHNWYTPNHVDQNKEPKNYYYYFNJHNJNHYYLKNILHI
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INNNNNNNNNNNIYIDINIQFYNKNYSCTHNNYIKNETNDNYPNSTIRNQHPNDQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="Mlfykliclflsfillingkdisstkkliksgnlank!kkgre
Ryggiynskymfiekrrkynyikkoknnnsyfsychvyknndynnnytaynyyinnp
Knklkeyyekiknhvikkkkkifslkfsqnkrekkkkyffinftsfhdikdulf
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LTFINYNNINESIQIIKLIGMLISVHKHNKLSPFHMNNLNVQNAANYLFKNLYNLQNI
QDLKKIEMMVYYDNLTFKFYKLFKNIISINVKRYVQNCNSYNKYEMVTHTNNLNKNEQ
                       NDIKTTVTAMKNKYNDOLLTTSYSNKKI DTVNASFOMAOSPEYIFLNIKFSHRWSSPGA
LKVKDEEIVSKKNNPSFSALSNDSNSVTKKYIVDLTLLDNIIESETKYNPASVGKVVV
TLKKEKKKIWNRLLLSKEKYPNMQVWWDMKEKRIHIITFVTINLFFLLSLSHRYHDSV
                                                                                          ONFLKEEKNNSDKLODDIDEDBEKYFDEELLREAKKKSEEYDKDDEEL"
complement (join110024 .10044,10320 .10336,10397 .10445,
10613 .10674,10773 .10798,10929 .10999,11157 .11237,
11453 .11515,11715 .11767,11950 .12040))
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DMTKKYKEGVDFLKESERRAQDIEDIGYTIMSELNSQRSAILRTKHHTDETRQEQNRV
       OKIFHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
                                                                                                                                                                                                                   complement(join(10024. 10044,10320. 10336,10397. 10445,
10613. 10674,10773. 10798,10929. 10999,11157. 11237,
11453. 11515,11715. 11767,11950. 12040))
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larity 46.7%; Pred. No. 0.00017;
Conservative 0; Mismatches 441; Indels 10;
                                                                                                                                                                                                                                                                                                                     note="Revised: new gene prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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db_xref="G1:3477015"
                                                                                                                                                                                                                                                                                         /gene="PFC0582c
                                                                                                                              gene
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                              linear
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Sequence 386 from Patent WO02077272.
AX599046
                                                                                                  AX599046.1 GI:28399186
                                                                                                                                               synthetic construct
synthetic construct
artificial sequences.
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28 AAAAGTTATTGGGCATTTTTTGAAAATAAAAAAAAATATCAATAAGTTGGAGTCATTACCGA

Similarity

Best Local Sim Matches 395;

Query Match

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                                      1. 8056
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/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                              Length 8056;
                                                                                                                                              9.5%; Score 90; DB 6; Length 805
46.0%; Pred. No. 0.00041;
ative 0; Mismatches 400; Indels
       WO 02077272-A 386 03-OCT-2002
Patent: WO Ozurra
Epigenomics AG (DE)
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AE014832 258658 bp DNA linear INV 07-OCT-2002 Plasmodium falciparum 3D7 chromosome 10 section 4 of 7 of the complete sequence.

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Plasmodium falciparum 3D7

Plasmodium falciparum 3D7

Plasmodium falciparum 3D7

Plasmodium falciparum 3D7

Eukaryorata; Alveodata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryorata; Alveodata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryorata; Alveodata; Apicomplexa; Haemosporida; Pann, A., Nelson, K.E., Bowman, S., Paulsen, I.T., Garlton, J.M., Pann, A., Nelson, K.E., Bowman, S., Paulsen, I.T., Amen, V., Shallom, S.J., L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Nather, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Railph, S.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McPadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Barrell, B.

Genome sequence of the human malaria parasite Plasmodium falciparum Nature 419 (6906), 498-511 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Location/Qualifiers
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AE014832.1 GI:23495046
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Gardner, M.J.
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186575 ATAAATAAATATATATATATATAATTAACATGATATTAATAAAGATAAATACAATAT 186634
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186635 TATAGCATTAAAATATAAATATAAAAATAAATAATAATAATACACATTATATATTTAAA 186694
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                                                                                                                                                                                                                                                                                             687
                                     TITAAGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAA 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
Methods and nucleic acids for the analysis of hematopoietic cell
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ABN92693 standard; DNA; 387

ABN92693 ID ABN9 RESULT 2

CGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAACTGAT TAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAGGAGGTTTACAAGA Disclosure; SEQ ID 2156; 267pp; English. gene; ds (GENO:) GENOME THERAPEUTICS CORP. gene therapy; 97US-055779F. 97US-064964P. 98US-0134001 ä Staphylococcus epidermidis Bush WPI; 2002-381255/41. Doucette-Stamm LA, P-PSDB; ABP40148 Staphylococcus antibacterial; 13-AUG-1998; 14-AUG-1997; 08-NOV-1997; US6380370-B1 30-APR-2002 345 465 9 285 120 180 405 240 ò g g g g ò ઠે  $\stackrel{>}{\circ}$ ð d à This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human disease, including callulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium. ö 333 393 120 453 180 513 240 573 9 Staphylococcus aureus in the production of Kunsch CA Fannon MR, rotymucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines AAAATTAACTTAAAATTTAAATATTGAAGA 390 Claim 1; Page 1984-1985; 3271pp; English Dillon PJ, Choi GH,

7; epidermidis; open reading frame; ORF; bacterial infection; CATCAATGATTTGGTTAATGCGACATTTCAAGTAAAAAATTTTTTTAGAGATACTAAAAA 119 344 179 404 239 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP3154 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

NB. The sequence data for this patent did not form part of the printed Specification, but was obtained in electronic format directly from the USPTO web site. 59 TAACGAAATCTCAACAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAAC 165 ACCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTTAATAATGAGTAAAATTAATGA 1 ACCTTGCTACAACAAGATGTGCATCAG-AGGAGTGGTTTTTATAATGGGAAAAATTAAAGA GAAGTTCAATTTGAACTATGAAGAAATTTATATTTTTAAATCATATTTTAAGAAGTGAGTC GCAATATAAATTTAAAATTAAGAAATTTATATTCTTAATCACATTTTGAAAAGTGAATC TAACGAAATATCTTCAAAAGAAATTGCTACATGTTCAGAGTTTAAACCGTATTATTTAAC 25 TATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAA Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections 1; Gaps Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2156 DB 24; Length 387; Indels Sequence 387 BP; 175 A; 39 C; 55 G; 118 T; 0. other; Query Match 27.6%; Score 261.4; DB 24; Best Local Similarity 81.4%; Pred. No. 4.2e-35; Matches 315; Conservative 0; Mismatches 71; 24-JUL-2002 (first entry) 

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Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
Pelet C, Schwope I, Ziebarth H;
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                                              360 TTTAGAATTAGAAACTATATCAAATA 386
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ABZ10246/c
ID ABZ10246 standard; DNA; 8056
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Score 96.2; DB 25; Length 8056; Pred. No. 1.4e-07;

10.2%;

Query Match Best Local Similarity

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G, Lesche R, Leu E;
Mueller V, Otto T;
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9.5%; Score 90; DB 25; Length 80
Best Local Similarity 46.0%; Pred. No. 1.6e-06;
Matches 341; Conservative 0; Mismatches 400; Indels
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Pelet C,
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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides. Haematopoietic cell proliferation disorder related DNA sequence #240. Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia; cytosine methylation state; gene; ds. Mueller J; e R, Leu E; G, Lesche R, Le Mueller V, Otto

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                                                                                           The present invention describes a method for detecting and discretes differentiating between hamalopoietic cell proliferative discretes associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CDG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cycosine methylation state and/or single nucleotide polymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cycosine methylation state and/or single nucleotide related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a pradisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-ollgomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
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                                                                                                                                                                       745 TAATATTTTCTTAGAAAATCAAGTTTACGATCATAAATATTTTCTGCGATATAGCTTTGG
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30-UUN-2000; 2000DE-1032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6292;
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Pred. No. 3.4e-05;
0; Mismatches 410; Indels
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in given. Invention describes a method for detecting and associated with at least 1 gene and/or their regulatory regions in a sociated with at least 1 gene and/or their regulatory regions in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the myelose sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation of haematopoietic cell proliferation also he myention can also be used for detecting a predisposition to, differentiation between a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders proliferative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller'J;
e R, Leu E;
, Otto T;
                                                                                                          Haematopoietic cell proliferation disorder related DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Howe A, Mueller
G, Lesche R, Le
Mueller V, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a method for detecting and
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45.5%; Pred. No. 6.7e-05;
tive 0; Mismatches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Braun A, Distler J, Guetig D, Piepenbrock C, Adorjan P, Grabs Lipscher E, Maier S, Model F, Schwope I, Ziebarth H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 28; SEQ ID 240; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002; 2002WO-EP03401.
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                                                              (first entry)
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Matches 368; Conservative
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                                                                 16-JAN-2003
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Pelet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K,
                   ABZ10100;
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ABZ10100 standard; DNA; 8056

ABZ10100/c ID ABZ101 RESULT

96US-0009861

35-JAN-1996;

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                           1373 ATTTTTAÄTAÄAAATTTTAAATTTAAATTTTTTTTTAAAATTATAÄAATTATÄAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                 AACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTTAACT
                                                                                                                                                                                                                                                                                                          GAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAACTGATT
                                                          ATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTTCAGAGATACAAAAAG
                                                                                       TATAATTTATTAATTTTAAAAAATATTACGTTTTTATATATTATATAATTACGTAACG
                                                                                                                                                                                                                                            AAAGCTTTACAAAAGCTAAAAAGATTTAAAAATTGTTATCAAAGAAAAAAAGAAGTTTACAAGAC
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CCTTGCTACAACAAGATGTGCATCAGAAGGAGTGGTTTAATAATGAGTAAAATTAATGAT
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S aureus infection. The polypeptides can also be used in a kit for the immunodetection of S aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can define the composition of the Staureus of the Staurences contained on the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
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                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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                                                          Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79.4; DB 18;
Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101 BP; 33 A; 20 C; 12 G; 35 T; 1 other;
                                                          Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9.76
0; Mismatches
                                                                                                                                                                                               English.
                                                          Dillon PJ,
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                           HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                               Claim 1; Page 2007; 3271pp;
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                                                        Choi GH,
                                                                                                    WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          computer readable
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08-NOV-1997;
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ID ABN92692
                                                                        Rosen CA;
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Matches
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Escherichia coli.
                                          USPTO web site
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                                                                                                      05-OCT-2000
                                                                                                                           03-AUG-2000
                                                                                                                                           Zyskind J,
                                                                                                  AAA66121;
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AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide adquences derived from Escherichia coli which inhibit E. coli proliferation. AAA6589 to AAA66055 and AAB15886 to AAB1600 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66050 to AFA6605 and AAA6605 to Septementing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention and be used to proliferation inhibiting nucleotide inserts in an example from the present invention can be used to a microorganism with a proliferation-required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTTGTTTAGAATGAACTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 CTATCAATAAGTTGGAGTCATTAACGACATTAAAAGTAACTTTTTTGAAATTAGAGAAAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GITITICAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCATTTTTTGAAAATAAAAA
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                                                                                                    Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.0%; Score 75.6; DB 21; Length 529;
Best Local Similarity 76.2%; Pred. No. 0.00041;
Matches 93; Conservative 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pUC19 promoter-terminator expression cassette SEQ ID 20.
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                                                                                                                                                                                                       Claim 1; Page 313; 316pp; English.
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                                                     WPI; 2000-514822/46.
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     Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            864 ACCATGTGGGCAATTGAGAAATAGCAACACGACAATCGGATGTATTGCTATAAGAACT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747 rccargadradgraarrdrgrgaraccrarrcracagrdgrdrrgrrrrrgaaarcagc 688
                                                                                                                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences an also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequence can be used to screen for compounds able to interfere with the S. epidermidis life Cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          744 ITAATATITITCITAGAAAATCAAGTITACGATCATAAATATITITCIGCGATATAGCTITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867 TTAATATTTTCTTAAGAAGTTAATTTGTCGATGATAAATCGTTTGATTGTTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807 AACACGAGTCAAAATTTCTTCTATTATTTGAGTTCTTTTAGTCAAAATACGAACGGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 GATGGTTCCAAGTATTTTCTCTATAATTTGTGTGCGATAAGCAAAATTCTAACTGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli, E. coli, proliferation, inhibition, screening, antimicrobial, bacterial growth, antisense therapy, antibacterial, ds.
                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77.6; DB 24; Length 867;
Pred. No. 0.00019;
0; Mismatches 79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL, Trawick J, Forsyth RA, Froelich JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 867 BP; 309 A; 146 C; 140 G; 272 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli proliferation inhibiting clone SEQ ID NO:468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
                                                                                                                                                                                                                                                 Disclosure; SEQ ID 2155; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           924 AATGGTTTCATAAACTGAATCGAT 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687 AACCGCGTGTAAATATCTTCTAT
(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%;
                                               Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA66121 standard; DNA; 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2000; 2000WO-US02200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0117405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.3
Matches 125, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
                                                                                               WPI; 2002-381255/41.
P-PSDB; ABP40147.
                                               Doucette-Stamm LA,
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Gaps ..

9

Example 11; Page 108-117; 182pp; German. gene from Phaeodactylum tricornutum

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This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (LI-P-SG-L2) in where Li = is a polylinker sequences reproduced (ABQ7629-ABQ7600) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing the EC, an organism containing the EC or the vector and a transgenic plant containing a fnon-) functional nucleic acid in the vector. Transgenic plant esq linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. protect against heart disease. The expression casettes of the invention protect against heart disease. The expression casettes of the invention protection in the blood and to protect against heart disease. The expression casettes of the invention (especially PUFA), including seed specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GITCICAAAATCGGIGGAGGGGGAIGAAGICAICGGGCAITAICIGAACAIAAAACA.3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic; animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTTTTCAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCATTTTTTGAAAATAAAAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
             New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 12079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12079 BP; 2835 A; 3149 C; 3385 G; 2710 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3689 czarcanakacircarcarracccaninarchia 3654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 75.2; DB 24
86.5%; Pred. No. 0.00045;
live 0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant specific expression vector SEQ ID NO 22.
                                                                                           Example 13; Page 112-121; 188pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV74271 standard; DNA; 12079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-2001; 2001DE-1002337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 86.5
les 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE10102337-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV74271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant;
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The invention relates to preparing (M1) fatty acid esters (I) with anomoreased content of polyunsaturated fatty acids (II) with at least two double bonds by introducing into a (I)-producing organism a specific nucleic acid (A). (M1) is useful for preparing ester containing to polyunsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and parmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. Cells that express (A) are also used to identify (ant)agonists of desaturases, e.g. for modulating the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as structural studies. (M1) is suitable for large scale production (no known structural studies. (M1) is suitable for large scale production (no known bloongineering method can produce (II) on a useful scale). The present sequence is that of a pucil based expression vector with a plant specific promoter and terminator surrounding the site for insertion of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3749 GTTCTCAAAATCGGTGGAGCTGCATGACAAGTCATCGGGCATTATCTGAACATAAAACA 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scheffler J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoter; expression cassette; structural gene; plant; transgenic; linesed; fetty acid ester; polyunsaturated fatty acid; PUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed-specific; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GITTICAAAATCGGIGGAGGIGCAIGAAAAAGIIAIIGGGCAITITITGAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparing
polyunsaturated
                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Score 75.2; DB 24; Length 12079;
86.5%; Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12079 BP; 2835 A; 3149 C; 3385 G; 2710 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drexler H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pUC19 promoter-terminator expression cassette SEQ ID 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New expression cassette for plant genes, useful for transgenic plants that have increased production of fatty acids - .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3689 CTATCAATAAGTTGGAGTCATTACCCAATTATGATA 3654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; Page 104-112; 188pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ76792 standard; DNA; 12085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-675961/73.
                                                                                                                                                                                                                                                                                                                                                                 expression cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE10102338-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ76792;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ76792/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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Zaehringer U;

Domerque F,

Heinz E,

WPI; 2002-644810/70. Lerchl J, Renz A,

(BADI ) BASF PLANT SCI GMBH

Preparing ester containing polyunsaturated fatty acids, useful e.g. animal or human nutrition, by transforming organism with desaturase

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invention
X888888888888888888888888888888888888
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This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (11-P-SG-12) in where it is a polylinker sequences reproduced (ABQ7799-ABQ7861) or equivalent RE-site-containing sequences reproduced (ABQ7799-ABQ7861) or equivalent RE-site-containing the EC or the vector and a transgenic plant on organism containing the EC or the vector and a transgenic plant EC, an organism containing the EC or the vector and a transgenic plant containing a mon-luncian nucleic acid in the vector. Transgenic plants et a linesed can be prepared with improved production of fatty acid esters with an increased content of polyumsaturated fatty acids (PUPA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention of the containing the provise in the production of fine chemicals. (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the

Sequence 12085 BP; 2838 A; 3149 C; 3385 G; 2713 T; 0 other;

· 0 3749 Gricicaaaarcegigeagciecareacaaagrcarcegecarrarcicaacaraaaca 3690 9 1 GITITICAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCCATTTTTTGAAAATAAAAA DB 24; Length 12085; ô 13; Indels 3689 CIATCAATAAGTIGGAGTCATTACCCAATTAIGATA 3654 61 ATATCAATAAGTIGGAGTCATTACCGAATTTTTATA 96 7.9%; Score 75.2; DB 2486.5%; Pred. No. 0.00045. Local Similarity 86.5 es 83, Conservative Query Match Best Loc Matches g 8 ò 엄

ABV74270 standard; DNA; 12085 

ABV74270;

(first entry) 28-MAR-2003

Plant specific expression vector SEQ ID NO 21.

Desaturase, fatty acid, ester, polyunsaturated fatty acid, cosmetic, animal nutrition, pharmaceutical, cholesterol, heart disease, transgenic, plant, ds.

Synthetic

DE10102337-A1

25-JUL-2002

19-JAN-2001; 2001DE-1002337.

19-JAN-2001; 2001DE:1002337.

(BADI ) BASF PLANT SCI GMBH

Zaehringer U; Domergue F, Heinz E, MPI; 2002-644810/70. Renz A, ۵, Lerchl

Example 11; Page 100-108; 182pp; German. animal or human nutrition, by transf gene from Phaeodactylum tricornutum

Preparing ester containing polyunsaturated fatty acids, useful e.g. animal or human nutrition, by transforming organism with desaturase

The invention relates to preparing (M1) fatty acid esters (I) with an increased content of polyunsaturated fatty acids (II) with at least two

double bonds by introducing into a (I)-producing organism a specific nucleic acid (A). (M1) is useful for preparing ester containing polyunsaturated fatty acids. Oils, lipids and (II) are their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. (Calls that express (A) are also used to identify (ant) agoinst so desaturases, e.g. for modulating the yield and rate of production of particular fine chemicals in microrganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (M1) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present sequence is that of a puct3 because expression vector with a plant specific promoter and terminator surrounding the site for insertion of an expression cassette \$

Sequence 12085 BP; 2838 A; 3149 C; 3385 G; 2713 T; 0 other;

Gaps 7.9%; Score 75.2; DB 24; Length 12085; 86.5%; Pred. No. 0.00045; . Ative 0; Mismatches 13; Indels 0; Local Similarity 86.5 nes 83; Conservative Query Match

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3749 GTTCTCAAAATCGGTGGAGCTGCATGACAAGTCATCGGGCATTATCTGAACATAAAACA 3690 1 GITITICAAAATCGGTGGAGGTGCATGAAAAGTTATTGGGCCATTTTTTGAAAATAAAAA 61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATA 96 В ઠે

3689 CTATCAATAAGTTGGAGTCATTACCCAATTATGATA 3654

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ABQ76791 standard; DNA; 12093 RESULT 15 ABQ76791/

ABQ76791;

(first entry) 25-MAR-2003

pUC19 promoter-terminator expression cassette SEQ ID 18.

Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed-specific, ds.

Synthetic

DE10102338-A1

25-JUL-2002.

19-JAN-2001; 2001DE-1002338. 

19-JAN-2001; 2001DE-1002338.

(BADI ) BASF PLANT SCI

Heinz E, Œ, Bischoff Lerchl J, Duwenig E, WPI; 2002-675961/73.

Scheffler J;

Drexler H,

preparing polyunsaturated New expression cassette for plant genes, useful for transgenic plants that have increased production of fatty acids

Example 13; Page 95-103; 188pp; German.

This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flamked by specific restriction enzyme (RE) recognition sites. The EC has the structure (II-P-SG-L2) In where II = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker

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sequences and n = 1-3. The invention discloses a vector containing sequences and n = 1-1. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a floor) functional nucleic acid in the vector. Transgenic plants e.g linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression casettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the
sequences reproduced (ABQ76799-ABQ76801) or equivalent RB-site-containing sequences and n = 1-3. The invention discloses a vector containing this
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Sequence 12093 BP; 2837 A; 3154 C; 3390 G; 2712 T; 0 other;

0; Gaps Query Match 7.9%; Score 75.2; DB 24; Length 12093; Best Local Similarity 86.5%; Pred. No. 0.00045; Matches 83; Conservative 0; Mismatches 13; Indels 0;

3749 GITCTCAAAATCGGTGGAGCTGCATGACAAAGTCATCGGGCATTATCTGAACATAAAACA 3690 

3689 CTATCAATAAGTTGAGTCATTACCCAATTATGATA 3654

61 ATATCAATAAGTTGGAGTCATTACCGAATTTTATA 96

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120 GCAATATAATTTAAATTATGAAGAAATTTATATTCTTAATCACATTTTGAAAAGTGAATC 179
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81.4%; Pred. No. 8.9e-46;
live 0; Mismatches 71;
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(GgDZ_6/ptodata2/ina/5A_COMB.seq:*
/GgDZ_6/ptodata2/ina/5B_COMB.seq:*
/GgDZ_6/ptodata2/ina/6A_COMB.seq:*
/GgDZ_6/ptodata2/ina/6B_COMB.seq:*
/GgDZ_6/ptodata2/ina/PCTUS_COMB.seq:*
/GgDZ_6/ptodata2/ina/PCTUS_COMB.seq:*
/GgDZ_6/ptodata2/ina/Packfiles1.seq:*
version 5.1.6
- 2003 Compugen Ltd.
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US-08-676-782-10
US-08-676-782-13
US-08-920-821-6
US-08-920-821-6
US-08-920-821-6
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US-08-920-821-6
US-08-920-828-6
US-08-938-416-2314
US-09-411-638-651
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Sequence 2155, Application US/09134001C

Sequence 2155, Application US/09134001C

Sequence 2155, Application US/09134001C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

SEQ ID NO 2156

LENGTH: 387
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Sequence 4, Application US/09948138
Sequence 4, Application US/09948138
Sequence 4, Application US/09948138
Sequence 4, Application US/09948138
GENERAL INFORMATION:
TITLE OF INVENTION: DEBNIFICATION AND CHARACTERIZATION OF A DWARF AND LATE FLOWERING
TITLE OF INVENTION: DEBNIFICATION AND CHARACTERIZATION OF A DWARF AND LATE FLOWERING
TITLE OF INVENTION: DEBNIFICATION WHERE: US/09/948,138
CURRENT FILING DATE: 2001-09-05
SEQUENCE FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PARCENTIN VERSION 3:0
SEQ ID NO 4
LENGTH: 12241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57302 GTTCTCAAAATCGGTGGAGCTGCATGACAAGGTCATCGGCCATTATCTGAACATAAAACA 57243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57242 CTATCAGTAAGTTGGAGTCATTACCTGAGAATAATACTCCTGGCTAAGTGAGCAGATAC 57183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTTTGTTTTAGAATGAACTTTA
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Best Local Similarity 50.5%; Pred. No. 2e-07;
Matches 188; Conservative 0; Mismatches 184;
                                                                                                                                                                                     NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
APPLICATION NUMBER: US/09/453,702B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                                                 APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                TELECONMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                         FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS
                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                 Sequence 2155, Application US/09134001C

Bedent No. 6380370

GENERAL INFORMATION:

APPLICANT: LIVEN BOUGETEE-Stamm et al

TITLE OF INVENTION: DYDERMINE ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DYDERMINES FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DYDERMINES FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR PLING DATE: 1998-08-13

PRIOR PLING DATE: 1997-08-14

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          807 AACACGAGTCAAAATTTCTTCTATTATTTGAGTTCTTTTAGTCAAAATACGAACGGCCAA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 ACCATGTGTAGGCAATTGAGAAATAGCAACACGACAATCGGATGTATTGCTATAAGAACT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747 recardadradricardadrectarreracidenterrerandenterringaaareac 688
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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 867;
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ZIF: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 77.6; DB 4;
Pred. No. 9.4e-08;
0; Mismatches 79;
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                                     360 TITAGAATTAGAAACTATATCAAATA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
TTCAGAATTAGAAGAATACATTAAAAA 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2155
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US-09-453-702B-57/c
; Sequence 57, Application US/09453702B
; Patent No. 6365723
; Patent No. 6365723
; Patent No. Frederick
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Best Local Similarity 61.3<sup>3</sup>
Matches 125; Conservative
                                                                                                                              RESULT 2
US-09-134-001C-2155/c
525
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144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 CAAAAACTGATTTCAGAAATTAGAAGAATACATTAAAAATTAAATCAAGGTTAATTGCGTT 573
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                                                                                                                                                                                      214 AAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGGTTAAGAAGTTTTCAGA
                                                                                                                                                 ö
                                                                                                        Length 447;
                                                                                                      Query Match 7.2%; Score 68.6; DB 4; Length 4 Best Local Similarity 49.3%; Pred. No. 6.1e-06; Matches 179; Conservative 0; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08676782

Sequence 10, Application US/08676782

Sequence 10, Application US/08676782

GENERAL INFORMATION

APPLICANT: FISCHETTI, Vincent A. TITLE OF INVENTION: REQUIATION OF EXOPROTEIN IN TITLE OF INVENTION: RAPHYLOCOCCUS AUREUS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. BOX 1404

STREET: Virginia States

STREET: Virginia States

ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,782 FILING DATE: 08-JUL-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION DATA: US/08/248,505 FILING DATE: 25-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERNCE/DOCKET NUMBER: 016921-092
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                    TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                US-09-134-001C-277
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  LENGTH: 447
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                                                                                                                                                                       1 GTTTTCAAAATCGGTGGAGGTGCATGAAAAAGTTATTGGGCATTTTTTGAAAATAAAAA 60
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7.9%; Score 75.2; DB 4; Length 13737;
Best Local Similarity 86.5%; Pred. No. 4.6e-07;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
                                                                                7.9%; Score 75.2; DB 4; Length 12241; 86.5%; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-09-538-414-10
                                                                                                                            0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                               10901 CTATCAATAAGTTGGAGTCATTACCCAATTATGATA 10936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Rendra, C.
APPLICANT: Rendra, D.
APPLICANT: Rendra, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Bill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist, US/O9/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 10
                                                                                                                                                                                                                                                       61 ATAICAATAAGTIGGAGTCAITACCGAATTITIATA 96
; TYPE: DNA
; ORGANISM: vector, multiple sequences
US-09-948-138-4
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09538414
Patent No. 6346655
GENERAL INFORMATION:
                                                                                                                            83; Conservative
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                                                                                    Query Match
Best Local Similarity
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US-09-538-414-10/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 393 base paire
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                                                                                                                                                                                                                                                                                                                             207 AATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTT
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                                                                                                                                                                                                                                7.1%; Score 67.2; DB 2; Length 1349; nlarity 49.2%; Pred. No. 1.4e-05; Conservative 0; Mismatches 183; Indels 0
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,505
FILING DATE: 24-MAY-1994
CLASSIFICATION: 435-5
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 016921-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFENDE: (703) 836-620
TELEFENDE: (703) 836-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: CHEUNG, Ambrose
APPLICANT: CHEUNG, Ambrose
TITLE OF INVENTION: REGILATION OF EXOPROTI
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTNS, Doane, Swecker & Mathi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08248505
Patent No. 5587288
                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                  LENGTH: 1349 base pairs
TYPE: nucleic acid
                                                                                                                   single
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                                                                                                                                                                                                                                                      Best Local Similarity
Matches 177; Conserv
                                                                                           TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                   US-08-676-782-10
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327 TATTITAAGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTT 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 CAAACAACCACAAGTTGTTAAAGCAGTTAAAATTTTATCTCAAGAAGATTACTTCGATAA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AAAAATCGAATCATTATTGAGTCGAGTAAATAAACGAATCACTGAAGCAAACAACGAAAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 GAAAAGATTTACAAGACGAAAGAACAGTTATTGTTTATGTTTACAGATACACAAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AATTACAAAATCAATGATTGCTTTGAGTTGTTATCAATGGTCACTTATGCTGACAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ITTCAGAGATACAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                207 AATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTT
                                                                                                                                                                                                                                                                                              Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
ONRESPONDENCE ANDRESS:
ADDRESSES: BURNES, 18
CORRESPONDENCE ANDRESS:
ADDRESSES: BURNES, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
STATE: Virginia
STATE: Virginia
STATE: Virginia
STATE: P.O. Box 1004
CONVIRY: United States
ZIP: P.O. Box 1004
CONVIRY: The PC companion STATE: P.O. Box 1004
CONVIRK: The PC companion STATE: P.O. Box 1004
CONVIRK: FIPPY disk
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PRANCE: PCDOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              Score 66; DB 1; Le
Pred. No. 2.1e-05;
0; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...к: US/08/676,782
08-JUL-1996
NN: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-08-676-782-6
Sequence 6, Application US/08676782
Patent No. 5976792
GENERAL INFORMATION:
                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.6%;
Matches 180; Conservative
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 TIGCGITIAA 576
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                                                                                                                                                                               CDS
19.390
                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-248-505-1
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Query Match
Best Local Similarity 46.3%;
Matches 296; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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US-08-487-826B-13

i Sequence 13, Application US/08487826B

j Patent No. 5993827

j GENERAL INFORMATION:
    APPLICANT: Sim, Kim i.
    APPLICANT: Chitnis, Chetan
    APPLICANT: Chitnis, Chetan
    APPLICANT: Peterson, David S.
    APPLICANT: Peterson, David S.
    APPLICANT: Willer, Louis H.
    APPLICANT: Bunding Chetan
    APPLICANT: Bunding Chetan
    APPLICANT: Bunding S.
    APPLICANT: Wellams, Thomas E.
    TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
    TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
    NUMBER OF SEQUENCES: 45
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Knobbe Martens Olson & Bear
    STREET: 620 Newport Center Drive 16th Floor
    CITY: Newport Beach
    STATE: California
    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266
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                 NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016921-092
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: GRANATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGT: 393 asse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              TOPOLOGY: linear _
MOLECULE TYPE: DNA (genomic)
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: CDS
; LOCATION: 19..393
US-08-676-782-6
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15410 ATTTATATTAAAAAAGAAATATAAAAACAAATTTATTAAAATGAAAAAAAGAAAAATGAA 15469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AAATAAAAAAATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTGTTTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ATGAACTTTATAACATAGTTGGATAGAGTTTTTCGATTTAATACATTAAATGTGAACCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 TGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531 ATTAGAAGAATACATTAAAAATTAAATTCAAGGTTAATTGCGTTTAATAACATTGAACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    591 AACAATTTATTAATACGAAGTTATTTATTCAGCATTGGGACATAAAATTAACTTAAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
CDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: US-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STRABLED NUMBER: 29,655
REGISTRATION NUMBER: NH121.001CP1
TELEFANCE/DOCKET NUMBER: NH121.001CP1
TELEFANCE/DOCKET NUMBER: NH121.001CP1
TELEFANCE (619) 225-8550
TELEFAX: (619) 225-856
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
TENNEYMENT: 19124 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65.4; DB 2;
Pred. No. 5.2e-05;
0; Mismatches 331;
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1878 ATAATTAAAAAGAATTCTCAATCAGCTTTCAAGAATTTGCAGTATTAACTTATATTAGT 1819
                                                                    1698 AATGAACACGATGAAAGAACTGTTTAATCTTAGTAGATTCTAAGCAGCGTAAAAAAATC 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1938 AAAATCAATGACTGCTTTGAATTATTAGCTATGGTCACTTATGCTGACAGATTAAAAGGA 1879
454 AGTTTACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GATACAAAAAGAAGTICAATITIGAACTATGAAGAAATITTATATITTAAATCATATITTA 333
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                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08920827

Patent No. 5770375

GENERAL INFORMATION:

APPLICANT: Ohno, Tsuneya

APPLICANT: Matsuhisa, Akio

APPLICANT: Uchara, Hirotsugu

APPLICANT: Uchara, Hirotsugu

APPLICANT: Uchara, Hirotsugu

APPLICANT: Uchara, Hirotsugu

APPLICANT: Uchara, Akio

APPLICANT: Uchara, Akio

APPLICANT: Uchara, Akio

APPLICANT: Uchara, Akio

STREET: Giolo Sears Tower, 233 South Wacker Drive

CITY: Chicago

CITY: United States of America

STATE: Illinois

COUNTRY: United States of America
                                                                                                                                                                                                  1638 GATGATTTACTTAAACGAGTAACAACGTATCACAGAAGGAATAATG 1590
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                                                                                                                                        514 CAAAAACTGATTTCAGAATTAGAAGAATACATTAAAAATTAAATCAAGG 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64.2; DB 1; Length 80
Pred. No. 8e-05;
0; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Staphylococcus epidermidis
Clinical Isolate SE-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19036/32420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
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APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTONEY/AGENT INFORMATION:
NAME: RID-LAULES, LI-HS-EN
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/920,827
29-AUG-1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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TELER: 25-3856
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
***NOTH: 8654 base pairs
****ACTEMBERS (Companies)
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Best Local Similarity 49.09
Matches 171; Conservative
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CLASSIFICATION:
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Patent No. 5763188
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Harshisa, Akio
APPLICANT: Ga, Soji
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Pred. No. 8e-05;
0; Mismatches 178; Indels 0
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   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLING DATE: 29-AUG-1997
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Clinical Isolate SE-22
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COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTOMNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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Best Local Similarity 49.0%;
Matches 171; Conservative (
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 8654 Dase pairs
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ADDRESSEE: Marshall,
STREET: 6300 Sears To
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MEDIUM TYPE: Floppy of
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EDNESS: double
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CLASSIFICATION:
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MOLECULE TYPE: (
ORIGINAL SOURCE:
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US-08-920-812-6/c
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878 ATAATTAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
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                                                                                        334 AGAAGIGAGICTAACGAAAICTCATCTAAAGAGAGATTGCTAAGTGCTCAGAGTTCAAACCT 393
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274 GATACAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTTA 333
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CITY: Chicago
STATE: Illiniad States of America
COUNTY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MR-1995
FILING DATE: 27-MR-1995
FILING DATE: 27-MR-1995
FILING DATE: 27-MR-1995
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Clinical Isolate SE-22
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GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bea, Soji
TILE OF INVENTION: Probe for Diagn
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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REGIESTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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Best Local Similarity
Matches 171; Conserve
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US-08-362-577C-6
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1758 CCTCAAGTTGTTAAAGCTGTTAAAAATTTATCTCAAGAAATTACTTTAATAAAAAACGT 1699
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                                              394 TACTATTTAACTAAAGCTTTACAAAAGCTAAAAAGATTTAAAATTGTTATCAAAGAAAAGA 453
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Pred. No. 8e-05;
0; Mismatches 178; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe for Diagnosing Infectious Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
CONTRY: United States of America
ZIP: 60606-6406
COMPUTER: ELOPPY disk
COMPUTER: ELD PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/921,177
FILLING DATE: 29-AUG-1997
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STRAIN: Clinical Isolate SE-22
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08921177 Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Welara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for INVENTION: Probe for INVENTION: APPRES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, STREET: Chicago Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 49.0%;
Matches 171; Conservative (
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nucleic acid
EDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
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STATE: Il
COUNTRY:
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US-08-921-177-6
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                                                 274 GATACAAAAAGGAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATCATATTTA 333
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920.828
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Clinical Isolate SE-22
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FILING DATE: 29-A0G-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-XAR-1995
ATTORNEY/AGENT INFORMATION:
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: United States of America
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ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-920-828-6/c; Sequence 6, Application US/08920828; Patent No. 5853998; GENERAL INFORMATION: APPLICANT: Ohno, Tsuneya
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REGISTRATION NUMBER: 33,547
REFRENCE/DOCKET NUMBER: 1903(
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312/474-630
TELEFAX: 312/474-630
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ohno, Tsuneya
APPLICANT: Meruhisa, Akio
APPLICANT: Ghara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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LENGTH: 8654 base pairs
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STRANDEDNESS: double
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STREET: 62.
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1878 ATAATTAAAAAAGAATTCTCAATCAGCTTTGAAGAATTTGCAGTATTAACTTATATTAGT 1819
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Length 8654;
Query Match
6.8%; Score 64.2; DB 2; Length 8
Best Local Similarity 49.0%; Pred. No. 8e-05;
Matches 171; Conservative 0; Mismatches 178; Indels
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November 17, 2003, 10:44:07; Search time 363 Seconds (without alignments) 8526.142 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 56, Appl Sequence 4, Appli Sequence 57, Appl Sequence 31, Appl Sequence 35, Appl	2444	ოთთოო	72 7 2 2 2 2 1	Sequence 12, Appli Sequence 1254, App Sequence 254, App Sequence 1026, Appl Sequence 182, Appl Sequence 182, Appl Sequence 182, Appl Sequence 182, Appl
US-09-845-064-56 US-09-810-861B-4 US-09-845-064-57 US-09-845-064-51 US-10-148-907A-35 US-10-148-907A-35	US-10-312-841-2 US-10-311-455-1190 US-10-311-455-2128 US-10-311-455-114	US-08-781-986A-253 US-10-311-455-1995 US-10-239-676-185 US-10-311-455-2331 US-10-311-455-933	US-10-055-001A-2 US-10-055-001A-2 US-10-055-001A-2 US-10-055-001A-2 US-10-055-001A-2	US-10-312-841.1 US-10-311-455-1258 US-10-311-455-254 US-10-311-455-1026 US-10-311-455-1026 US-10-311-455-182 US-10-311-455-182
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## ALIGNMENTS

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RESULT 1

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USCHARIAT PROGRATION
USCOROSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN TILLE OF INVENTION: DATE: 2001-01-1
USCHERNY PELLOATION WINGRER: US 60/261,233
PRIOR FILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-12
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PRIOR APPLICATION UNMER: US 60/289,601
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661 AGATGCTTTAATTAAAGTTAAAGACCAGCCATACCTTATTTCAGCTTATTAAGCTTGACA
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                                                                                                               <u>AACGCAACATTTCAAGTTAAGAAGTTTTTCAGAGATACAAAAAAGAAGTTCAATTTGAAC</u>
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                                                TAACATAGTTGGATAGAGTTTTCGATTTAATACATTAAATGTGAACCTTGCTACAACAAG
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US-10-043-539-19
Sequence 19, Application US/10043539
Sequence 19, Application US/10043539
Publication No. US20330114650A1
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Zhang, GONGYi
TITLE OF INVENTION: CONPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS;
TITLE OF INVENTION: BACTERIA
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COMPUTER READABLE FORM:
MEDLIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vecira 486/33
COMPUTER: HP Vecira 486/33
COPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII TEAC.
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 03/08/781,986A
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 30,446
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: 30,446
RECISTRATION NUMBER: 30,966
TELECOMMUNICATION INPREMATION:
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; STRANDEDNESS; double
; TOPOLOGY: linear
US-08-781-986A-1525
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Matches 388;
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US-08-781-986A-1525
US-08-781-986A-1525
Sequence 1525, Application US/08781986A
Sequence 1525, Application No. US20030054436A1
PUBLICATION No. US20030054436A1
SENERAL INPORMATION:
TITLE OF INVENTION: Standylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville

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Publication No. US20330054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                             <u>AATAATGAGTAAAATTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAA</u>
                                                                                                                                                                                                                   TCATATTTTAAGAAGTGAGTCTAACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGA
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                                                                                                                                     GTTTTTCAGAGATACAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage. COMPUTER: HP Vectra 486/33
COMPATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCELI Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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REGISTRATION NUMBER: 30,446
REFERENCE POCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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US-08-781-986A-1599/c
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Fublication No. US2030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
ITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des )
FILE REFERENCE: E01/1208/NO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                           DB 14; Length 210; 2e-26;
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                                                                                                                                                                                                                                                                                                                                                                    Indels
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22.2%; Score 210; DB
Best Local Similarity 100.0%; Pred. No. 2e-
Matches 210; Conservative 0; Mismatches
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          CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT FILING DATE: 2002-01-11
PRIOR PELING DATE: 2002-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PACENTIN VERSION 3.1
SEQ ID NO 19
LENGTH: 210
TYPE: DNA
CREANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Matches 327; Conservative
REFERENCE: DC-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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LENGTH: 3673778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ACTNATTIGITIAGAATGAACTITATAACATAGTIGGATAGAG-TITCGATTIAATAAAT
                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                      8.4%; Score 79.4; DB 8; Length 101; 92.2%; Pred. No. 0.00015; ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burland, Valerie
Perna, Nicole T.
Plunket, Guy
Plunket, Guy
Welch, Rod
TITLE OF INVENTION: NO US20030023075Alel Sequences of NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 TAAATGTGAACCTTGCTACAACAAGATGTGCATCAGAAGGAG 197
                                                                                                                                                                                                                                                                                                                                                                                                                          96 ACTTATTTGTTTAGAATGAACTTTATAACATAGTTGGATAGAGTT
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REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01.Apr-2002
CLASSIFICATION: <un>

CLASSIFICATION: <un>
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FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-114-170-57/c
Sequence 57, Application US/10114170
Sequence 10. US20030023075Al
CENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 87563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
TELEFAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 101 base pairs
                                                                                               LENGTH: 101 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-1599
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 94; Conser
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                                                                                                                                                                                                                                                                                                Query Match
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Length 87563;

DB 14;

8.2%; Score 77.6;

Query Match

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57302 GIICICAAAAICGGIGGAGCIGCAIGACAAGGICAICGGGCAIIAICIGAACAIAAAACA 57243
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                                                                                                                                                                                                                                                       61 ATATCAATAAGTTGGAGTCATTACCGAATTTTTATACTTATTTGTTTAGAATGAACTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                       121 TAACATAGTIGGATAGGAGTITICGATTTAATACATTAAATGTGAACCTIGCTACAACAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TATGAAGAAATTTATATTTTAAATCATATTTTAAGAAGTGAGTCTAACGAAATCTCATCT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-LILOUANDESCRIPTION:
Sequence 113786, Application US/10027632
Publication No. US20030204075A9
Fublication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR FLILNG DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1080-03-29
FRIOR FILING DATE: 1080-03-29
FRIOR FILING DATE: 1099-11-23
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ed. No. 0.0024;
Mismatches 184; Indels
       Pred. No.
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   Best Local Similarity 50.5
Matches 188; Conservative
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US-10-027-632-113786
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Best Local Simi
Matches 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATAAAGATTATTAGTATTAATGTAATAATTAAGCTTTTTAATATAAGTTATA 2124
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                                                                                                                                                                                                                                                                                                                            401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGAACGATAACAATTTAATACGAAGTTATTTATTCAGCATTGGGACATAAAATTAA 641
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TIGITIAGAAIGAACTITATAACATAGITGGATAGAGITITICGAITTAATACATTAAAIG 161
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US-10-027-612-113787

is Sequence 113787, Application US/10027632

is publication No. US20030204075A9

is GENERAL INFORMATION:

is APPLICANT: Wang, David G.

it TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION: Polymorphisms in the Human Genome

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it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION: Polymorphisms in the Human Genome

it TITLE OF INVENTION NUMBER: US 60/198,676

it PRIOR FILING DATE: 2000-04-20

it PRIOR FILING DATE: 2000-04-20

it PRIOR FILING DATE: 2000-03-29

it PRIOR FILING DATE: 2000-03-24

it PRIOR FILING DATE: 2000-02-24
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Pred. No. 0.0013;
0; Mismatches 444;
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-02-8
PRIOR PELLING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FaetSEQ for Windows Version 4.0
LENGTH: 3252
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Local Similarity 45.0%;
es 368; Conservative (
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US-10-027-632-113787
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Matches 368
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APPLICANT: Wandliow:
APPLICANT: Wandliow:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2000-07-12
PRICR PILING DATE: 2000-07-12
PRICR PILING DATE: 2000-04-20
PRICR APPLICATION NUMBER: US 60/198,676
PRICR APPLICATION NUMBER: US 60/193,483
PRICR PILING DATE: 2000-03-29
PRICR APPLICATION NUMBER: US 60/193,383
PRICR PILING DATE: 2000-02-34
PRICR FILING DATE: 12000-02-24
PRICR PILING DATE: 12000-02-24
PRICR PILING DATE: 1999-11-23
PRICR APPLICATION NUMBER: US 60/166,358
PRICR APPLICATION NUMBER: US 60/166,358
PRICR APPLICATION NUMBER: US 60/146,002
PRICR PILING DATE: 1999-09-28
PRICR PILING DATE: 1999-09-08
SPRICR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SCOFWARE FEASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                        42 ATTITITGAAAATAAAAATAICAAIAAGIIGGAGICAIIACCGAAIIIIIAIACTIAI
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45.0%; Pred. No. 0.0013;
ive 0; Mismatches 444;
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US-10-027-632-113786
; Sequence 113786, Application US/10027632
; GENERAL INFORMATION:
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US-10-027-632-113786
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                                                                                                            GENERAL INVENTION:

GENERAL INVENTION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10882.108/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PELING DATE: 2002-04-30

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

PRIOR PELING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FEELESCY for Windows Version 4.0

SEC ID NO 113798
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                                         Sequence 113788, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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US-10-027-632-113788
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Sequence 113787, Asplication US/10027632
GENERAL INFORMATION:
FAPPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: 10 Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: 10 Polymorphisms in the Human Genome
TITLE OF INVENTION: 10 Polymorphisms in the Human Genome
FILING DATE: 2002-04-30
PRIOR PELLING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-00-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE FRAILSE 
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; ORGANISM: Human
US-10-027-632-113787
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                                                                                  42 ATTITITGAAATAAAAAATAICAATAAGTIGGAGICATTACCGAATTITTATACTTAT
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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    Length 3252
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                                           0; Mismatches 444;
Score 76.6; DB 13;
Pred. No. 0.0013;
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Conservative
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Best Local Similarity
Matches 368; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 GATTICAGAATTAGAAGAATACATTAAAATTAAATCAAGGTTAATTGCGTTTAATAACA 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 TGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTCAGAGATACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AAAGAAGTICAATTTGAACTATGAAGAAATTTATATATTTTAAATCATATTTTAAGAAGTGA
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45.0%; Pred. No. 0.0013;
ive 0; Mismatches 444;
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: -1999-09-28
PRIOR FILING DATE: -1999-09-28
PRIOR FILING DATE: -1999-09-28
PRIOR FILING DATE: -1999-09-28
PRIOR FILING DATE: -1999-09-09
PRIOR FILING DATE: -1999-09-09
PRIOR FILING DATE: -1999-09-09
PRIOR FILING DATE: -1999-09-09
PRIOR FILING DATE: -1999-08-09
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Best Local Similarity 45.0
Matches 368; Conservative
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ORGANISM: Human
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APPLICANT: Greenlee, Winner and Sullivan, P.C.
APPLICANT: JOHN, Peter C.L.
APPLICANT: JOHN, Peter C.L.
APPLICANT: JOHN, Peter C.L.
APPLICANT: SEX, Francis J.
APPLICANT: SEX, Francis J.
APPLICANT: SEX, Francis J.
APPLICANT: VAN CAMP, Wim J.
TITLE OF INVENTION: CYCLE CONTROL PROTEIN
FILE REPERBNCE: DOCKET 19-00A
CURRENT APPLICATION NUMBER: US/10/122,085A
CURRENT FILING DATE: 2002-04-10
PRIOR FILING DATE: 2000-02-25
                                                  2185 ATATTATAATGTATTATATATTAAATTTAATATATAACTTATTCATATGTTACCATACA 2244
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Frosyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1 COLI
FILE REFERENCE: ELITRA.001DV1 COLI
FILE REFERENCE: ELITRA.001DV1 COLI
FILE REPERENCE: ELON-03-01-07-23
CURRENT APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SEQ ID NO 468
FILING DATE: 2006-01-27
NUMBER OF SEQ ID NOS: 485
SEQ ID NO 468
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Pred. No. 0.0011;
0; Mismatches 29; Indels
                                                                                                                                                                   2245 CAGTTAATATATATACAGTATAAACATATTAAACT 2281
                                                                                                                                                                                                                                                                                               Sequence 468, Application US/09912020
Patent No. US20020045592A1
GENERAL INFORMATION:
APPLICANT: Syskind, Judith
APPLICANT: Chisen, Kari L.
APPLICANT: Trawick, John
APPLICANT: Freelich, Jamie M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10122085A Publication No. US20030172404A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.2%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Escherichia coli
US-09-912-020-468
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US-09-912-020-468/c
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RESULT 15

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7.9%; Score 75.2; DB 13; Length 12241;
Best Local Similarity 86.5%; Pred. No. 0.0034;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                 Query Match
7.9%; Score 75.2; DB 12; Length 11777;
Best Local Similarity 86.5%; Pred. No. 0.0033;
Matches 83; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITITCAAAATCGGTGGAGGTGCATGAAAAAGTTATTGGGCATTTTT
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                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Cloning vector pBin19
US-10-122-085A-5
                     PRIOR FILING DATE: 1999-02-26
PRIOR PELING DATE: 1999-02-26
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 5
LENGTH: 11777
PRIOR APPLICATION NUMBER: US 60/121,870
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial
FEATURE:
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November 17, 2003, 09:13:37; Search time 2414 Seconds (without alignments) 9534.523 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_esthum...
em_estpl...
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em_brc...
gb_estl...
gb_estl...
gb_estl...
em_gss_hum...
em_gss_lnvv...
em_gss_
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Maximum DB seq length: 200000000
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947
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Perfect score:
Sequence:
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AL069706 Drosophil BX415878 BX415878 BX415878 BX415878 BX415058 BX415058

CNS00EVL BX415878 BX415878 BX415058

12.1 11.5 10.6

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Description

Query Match Length DB ID

Score

Result No.

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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP from the and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                      /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BARCR2923"
/clone lib="RRCI-98"
/note="end : T7"
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BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YI04 5-PRIME, mRNA sequence.

LOCUS DEFINITION

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/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pcNVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 170 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Library Email : fliang@allfetech.com U
http://fulllength.invitrogen.com/ EnvironGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPOOSBE02QP1.
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                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelu
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 1200)
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                                                                                                                                                                                          Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008Y104"
GI:30765550
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1056 bp mRNA linear EST 15-MAY-2003
B-X115058 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004YG19
BX415058
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1057 AWWAAAAWTWTAAWAAAATAATTTTTTTTTTAWAWWAAATAWAWTTTAWAWWTWWA 998
                                                                                                                                                                                                                                                                                                                                                                                                                            817 AAWITITITITATITITGIWATIWIWAAAITATITAWIAWAWIWAITITITATGHWIAITI 758
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Franche BP 191 91006 EVRY cedex - Franche BP 191 91006 EVRY cedex - Franche BP 191 91006 EVRY cedex - Franche BP 191 9100 EVRY was constructed by Life Technologies, a division of Library was constructed by Life Technologies, a division of Intitrogen. Contact : Feng Liang Email : fliangelifetech.com URL http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO04AD10NP1.
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Catarrhini; Hominidae; Homo.
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                                                                                       TITIAAGAAGIGAGICIAACGAAAICICAICIAAAGAGAIIGCIAAGIGCICAGAGIICA
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Mammalia, Eutheria, Primates,
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Homo sapiens
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/mol_type="mRNA"
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1 (bases 1 to 1200)
1 (Jam. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
Brail 91006 EVRY cedex - France
Email: Segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulllength.inviroscope.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAPOOBBECO20P1.
Location/Qualifiers
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                                                     AGGITAATTGCGTTTAATAACATTGAACGATAACAATTTTATTAATACGAAGTTATTATT
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Homo sapiens
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/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and BcoRV sites of the pcMvSPORT 6 vector.
Library was not normalized."
Library was not normalized."
175 others
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                                                                                                                                                                                                                                                                                                              GAAGTTTTTCAGAGATACAAAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>AAAAGCAAATATTCAAAAACTGATTTCAGAATTAGAAGAATACATTAAAATTAAATCAA</u>
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                                                                                                                10.5%; Score 99.8; DB 13; Length 1056; 36.3%; Pred. No. 0.00042; ive 106; Mismatches 378; Indels 6;
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Drosophila melanogaster genome survey sequence TET3 end of BAC #BACROBKIO of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

LOCUS

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- Web: www.genoscope.cns.fr

- Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named REDI-98 and was constructed by partial EcoxI digestion of Drosophila DNA, provided by the BDGP from the isogenic strain v2; no bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be botain.com.in.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="teaxon:7227"
/clone="BACROBK10"
/clone lib="RRCI-98"
/note="end : TET3"
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// Organishis rows...
// Ab_xref="uaxon:9606"
// Ab_xref="uaxon:9606"
// Cone="CSODEO14YFO3"
// Lissue type="PlaCENTA"
// Clone lib="Homo sapiens PlaCENTA"
// Clone lib="Homo sapiens PlaCENTA"
// Inche="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not! orly primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3370.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgibin/cluster.cgiseq=CSODEO14CCO3NP1&cluster=3370.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
Faraday Avenue Genoscope sequence ID: CSODEO14CCO3NP1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
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BP 191 91006 EVRY cedex - France
BEMail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 534.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSOCAPF008BD12NP1&cluster=534.r. Contact :
Feng Liang Email : fliang@lifetech.com URL : Contact :
http://lullengph.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPF008BD12NP1.
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/clone_Tib="Homo sapiens THYMUS"
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
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1...1045
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|Library was not normalized."|
| Library was not normalized."|
| Signature | 140 g | 441 t | 96 others |
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                                                                                                                                                                                                                                                                                                        10.3%; Score 97.4; DB 13; 44.4%; Pred. No. 0.00087; ive 36; Mismatches 344;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamalia, Eutheriz, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1045)

BX456814.1 GI:31034806

BX456814

ACCESSION VERSION KEYWORDS SOURCE

Homo sapiens (human)

Homo sapiens

ORGANISM

REFERENCE

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EST
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JOURNAL
COMMENT
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/mol_type="mRNA"

/db_txfe="txxxn:9606"

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with a Not!-oligo (dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

15 a 30 c 71 g 310 t 274 others
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Homo sapiens cDNA clone CS0CAP008YB01
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                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo. Li Dases, 1 to 1200)
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirogen. Contact : Feng Liang Email : fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO08CAO1QP1.
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llarity 30.4%; Pred. No. 0.001;
Conservative 170; Mismatches 365;
                                                                 903 GGATGTATTGCTATAAGAACTAATGGTTTCATAAACTGAA
                                                                                                                                                                                   1200
BX437758 Homo sapiens THYMUS
5-PRIME, mRNA sequence.
BX437758. GI:30773605
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/tissue type="B CELLS (RAMOS CELL LINE)"
/cell line="RAMOS CELL LINE"
/clone lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVEY cedex - France
BEMAIL: Sequence Genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Linvitrogen. This sequence belongs to sequence cluster 24.rr Corr mo
Library Library Radio Library Sequence Construction 1600
Faraday Avenue Genoscope sequence ID : CSODGOO4CA022PI.

Location/Qualifiers
                                                                                                                                                               TTAWAWWTATRARGADTTTTTTATAWWTATTTTTWWAWAAGATDKAAAAWWWTT
                                                       564 ITTITWWIWAWAAAASAGAWKAIWITITKKITIAIWWKRAGGAIWITITITIWIWAAR
                                                                                                                                                                                                                                                         466 GAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATTCAAAAAACTGATT
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346 AACGAAATCTCATCTAAAGAGATTGCTAAGTGCTCAGAGTTCAAACCTTACTATTAACT
                                                                                                                            406 AAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTTATCAAAGAAAAAAAGAAGTTTACAAGAC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/db_xref="taxon:9606"
/clone="CS0DG004YB03"
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BX420717 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF033YC10 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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   vector.
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0
                                                             Length 1201;
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   PCMVSPORT
                           others
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  the
                                                             ; Score 93.8; DB 13;
; Pred. No. 0.0025;
48; Mismatches 341;
the Not I and EcoRV sites of
Library was not normalized."
141 c · 153 g 522 t
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BX420717.1 GI:30658996
                                                           5ch 9.9%;
al Similarity 40.9%;
269; Conservative 4.
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Homo sapiens
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Matches
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/organism="Homo sapiens"

/mol_type="mRNA"

/do=faxon:9606"

/dlone="CSODF033YC10"

/tissue_type="FETAL BRAIN"

/dev_stage="FETAL BRAIN"

/dev_stage="FETAL BRAIN"

/dlone="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

85 a 115 c 108 g 299 t 94 others
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF033BB05QP1.
Location/Qualifiers
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9.8%; Score 93.2; DB 13;
Best Local Similarity 42.4%; Pred. No. 0.003;
Matches 271; Conservative 52; Mismatches 311;
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RESULT 12 AL536104/c

Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 TTAATGATATTAATGATTTAGTCAACGCAACATTTCAAGTTAAGAAGTTTTCAGAGATA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CSODF022YC18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primatee, Catarrhini, Hominidae, Homo.

1 (Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Li, W.B., Gruber, C., Jessee, J. and normalization

Unpublished

On Feb 13, 2001 this sequence version replaced gi:12799597.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 CAAAAAAGAAGTTCAATTTGAACTATGAAGAAATTTATATTTTAAATTTTAAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930 WATTWWWWAWAATWWTWTAWAAWTTATAAATAAAAWATAAAWTTAAAATTAAAAWAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 TACAAGACGAAAGAACAGTTATTGTTTATGTTACAGATACACAAAAAGCAAATATT-CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      517 AAACTGATTTCAGAATTAGAAGAATACATTAAAATTTAAATCAAGGTTAATTGCGTTTAA
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                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
EP 191 91006 EVRY cedex - France
Email: sequenceçec.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF022BB09QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.8%; Score 92.8; DB 9; Length 1
Best Local Similarity 35.1%; Pred. No. 0.0034;
Matches 197; Conservative 106; Mismatches 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not normalized.
409 t 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                            AL536104.2 GI:31260974
                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                 Contact: Genoscope
                                                                                                                                     Homo sapiens
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ORIGIN
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Gossyptum arboreum
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Gossyptum arboreum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Itacheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
jeurosids II; Malvales; Malvaceae; Malvoideae; Gossyptum.
I (Bases II to 887)
Mung, R. A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
Of the cotton fiber
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/note="Wector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
71 c 37 g 321 t 29 others
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697 TATTICAGCITATIAAGCITGACACAAGGIACACIAGICTITITATITITAATATITITCIT
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Pred. No. 0.0044;
0; Mismatches 296;
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Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High-quality sequence start: 2
High quality sequence stop: 881.
Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                           27 AAAAAGTTATTGGGCATTTTTTGAAAATAAAAAAATATCAATAAGTTGGAGTCATTACCG
                                                                                                                                                                        915 ААТААСААТААТААТААААТАААТАААТТТААААТААААТАААААТАААТАААТААА
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                                                                                                                 11;
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    This is a Xenopus Gene
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                                                                                Score 92.2; DB 14;
Pred. No. 0.0041;
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 Technologies. Note:
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(bases 1 to 1123)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                           441 ATCAAAGAAAAGAAGTTTACAAGAAGGAAGAACAGTTATTGTTTATGTTACAGATACACA
                                                                                                                      AAAAGCAAATATTCAAAAACTGATTTCAGAATTAGAAGAATACATTAAAATTTAAATCAA
81 AGAGTTCAAACCTTACTATTTAACTAAAGCTTTACAAAAGCTAAAAGATTTAAAATTGTT
                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Linn at:
Plate: Liamise lin. Gov
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High quality sequence start: 49
High quality sequence start: 49
Location/Qualifiers
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Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: Capabs-remail.nih.gov
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/organism="Xenopus laevis"
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CD325190/c
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AUTHORS
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| organism="Homo sapiens" |
| mol Lype="mRNA" |
| db xref="taxon:9606" |
| clone="CSOCAP008YB01" |
| tissue type="HYMUS" |
| clone Tib="Homo sapiens THYMUS" |
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Contact: Genoscope
Contact: Genoscope
- Centre National de Sequencage
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BR 191 91006 And Advision of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO08CA01QP1.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hoi
1 (bases 1 to 1200)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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open reading frame; ORF; bacterial infection;
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US6380370-B1
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interfere with the expression of the toxins, thereby functioning as antimicrobial agents to render the microorganism avirulent. The DNA encoding this sequence can be used for diagnostic identification of pathogenic staphylococci which express the protein, and the resulting virulence factor.

Local Similarity

Query Match

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polypeptide, useful for diagnosing and treating bacterial infections
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                                                     ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP31544 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated staphylococcal accessory regulatory protein and gene used to develop prods. for use as antimicrobial agents and for detection of pathogenic staphylococci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 486; DB 23;
Pred. No. 3.2e-40;
8; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcal accessory regulatory A protein.
Disclosure; SEQ ID 4993; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 9-10; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW14000 standard; Protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial endotoxin;
antimicrobial agent.
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N-PSDB; AAT60281.
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les 96; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                accessory regulatory procein (TI), designated sar) which regulates the expression of S. aureus exoprotein virulence determinants (EVD). (I) controls the expression of virulence determinants such as endotoxins in S. aureus. (I) is used to design analogs that interfere with expression of EVD, i.e. potential antibacterial agents and for generating specific antibodies which are used to detect (I) in microbial isolates or for affinity purification of (I). The nucleic acid (II) that encodes (I) or its fragments) can be used to identify S. aureus that express sar (and thus EVD) by usual hybridization and amplification tests, also for recombinant production of (I). This sequence represents the Expression of EVD and thus sequence represents the EXT of the method of Staphylococcus aureus sarA protein which is described in the method of
                                                                       9
                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New accessory regulatory protein, sar, from Staphylococcus aureus, used to design analogs potentially useful as antibacterial agents
                                                                     1 MSKINDINDLVNATFOVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
                                                                                           Staphylococcal accessory regulatory protein; sar protein; endotoxin; exoprotein virulence determinant; EVD; antibacterial agent; detection.
                                     Gaps
                                                                                                                                          61 KPYYLTKALOKLKOLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                              63 KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel full-length Staphylococcus aureus
                                   ô
                                   Indels
                                   52;
25.8%; Score 148; DB 18; 30.1%; Pred. No. 5.6e-07; iive 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 25-28; 30pp; English
                                                                                                                                                                                                                                                                  AAY50721 standard; Protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0676782
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                                   34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        S. aureus sarA protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
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N-PSDB; AAZ24204.
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DB 21; Length 124;

25.8%; Score 148;

Query Match

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17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel full-length Staphylococcus aureus accessory regulatory protein ((I), designated sar) which regulates the expression of S. aureus exoprotein virulence determinants (EVD). (I) controls the expression of virulence determinants (EVD). (I) in S. aureus. (I) is used to design analogs that interfere with expression of EVD, i.e. potential antibacterial agents and for generating specific antibodies which are used to detect (I) in microbial isolates or for affinity purification of (I). The nucleic acid (II) that encodes (I) or its fragments) can be used to identify S. aureus that express sar lend thus EVD) by usual hybridization and amplification tests, also for recombinant production of (I). This sequence represents a Staphylococcus aureus sarA protein which is described in the method of the invention.
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                                       1 MSKINDINDLVDATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sar, from Staphylococcus aureus, used
                                                                                                                                                                                                                                                                                             Staphylococcal accessory regulatory protein; sar protein; endotoxin; exoprotein virulence determinant; EVD; antibacterial agent; detection.
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                                                               3 ITKINDCFELLSMVTYADKLKSLIKKEFSISFEFFAVLTYISENKEKEYYLKDIINHLNY
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                                                                                          61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New accessory regulatory protein, sar, from Staphylococcus au
to design analogs potentially useful as antibacterial agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
              52; Indels
                                                                                                                                                                                                                                                                   S. aureus sarA protein fragment from strain RN450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.8%; Score 148; DB 21; Best Local Similarity 30.1%; Pred. No. 5.6e-07; Matches 34; Conservative 27; Mismatches 52;
5.6e-07;
30.1%; Pred. No. 5.6e tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Column 31-32; 30pp; English.
                                                                                                                                                                                     AAY50725 standard; Protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0676782
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               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fischetti VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SIGA-) SIGA PHARM INC.
                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-021938/02.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1994;
                                                                                                                                                                                                                                        08-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheung A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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The present sequence is given in a specification relating to a method for identifying inhibitors of SarA (staphylococcal accessory regulator) function involved in the expression of Staphylococcal virulence genes. The method comprises contacting a candidate inhibitor with a SarA binding site of the agr (accessory gene regulator) locus in solution binding site of the agr. The identified inhibitor to the SarA binding site of the agr locus. The identified inhibitors are useful for preventing and treating staphylococcal infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulator)
comprises
                                                                                                                                                                                                             Staphylococcus aureus; SarA; staphylococcal accessory regulator A; agr; accessory gene regulator; antibacterial; SarA inhibitor; virulence gene; staphylococcal infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying inhibitors of staphylococcal SarA (accessory regulato) which are useful for treating staphylococcal infections, comprises using specific binding sites of SarA protein on an accessory gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.8%; Score 148; DB 22;
ilarity 30.1%; Pred. No. 5.6e-07;
Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rechtin TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. epidermidis sarA protein fragment.
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  Ä.
                                                                                                                                                                 Staphylococcus aureus SarA protein.
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AAB68760 standard; protein; 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2000; 2000WO-US18525.
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                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulator locus
                                                                                                                                                                                                                                                                                                                                                                                        WO200103686-A2.
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ID AAY5
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This invention describes a novel full-length Staphylococcus aureus accessory regulatory protein ([1], designated sar) which regulates the expression of S. aureus exoprotein virulence determinants (EVD). (I) controls the expression of virulence determinants such as endotoxins in S. aureus. (I) is used to design analogs that interfere with expression of EVD, i.e. potential antibacterial agents and for generating specific antibodies which are used to detect (I) in microbial isolates or for affinity purification of (I). The nucleic acid (II) that encodes (I) or its fragments) can be used to identify S. aureus that express sar (and thus EVD) by usual hybridization and amplification tests, also for recombinant production of (I). This sequence represents a Staphylococcus aureus sarA protein which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New accessory regulatory protein, sar, from Staphylococcus aureus, used to design analogs potentially useful as antibacterial agents -
   exoprotein virulence determinant; EVD; antibacterial agent; detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.4%; Score 146; DB 21; Length 113; 29.7%; Pred. No. 7.9e-07; tive 27; Mismatches 51; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Column 31-34; 30pp; English.
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                                                             Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                       (SIGA-) SIGA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-021938/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA;
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                                                                                                                                                                                                                                                                                                                            24-MAY-1994;
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                                                                                                                           JS5976792-A
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 KIDSIFNTIKKKYGMSKEEILILLLLL--EKGSMTLKEMDKYVHIKPYKRTRTYNNLVNL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis; SarA; staphylococcal accessory regulator A; agr; accessory gene regulator; antibacterial; SarA inhibitor; virulence gene; staphylococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDL
                                                                                                                                                        Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : |: | | | | | | | | | | : | | : | | EWIYKERPQDDERTVIIHFNDKQNSKKEDLLKFIDDSIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.3%; Score 145; DB 23; Best Local Similarity 33.3%; Pred. No. 1.4e-06; Matches 33; Conservative 22; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis SarA protein.
                                                                                                                                                                                                             Disclosure, SEQ ID 5151; 267pp; English.
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                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB68761 standard; protein; 124
97US-064964P.
                                                                     Bush D;
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                                                                   Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 AA;
                                                                                                                       N-PSDB; ABN92851
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08-NOV-1997;
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Staphylococcus antibacterial;
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                                                Sequence
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Matches
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                                                     The present sequence is given in a specification relating to a method for identifying inhibitors of SarA (staphylococcal accessory regulator) function involved in the expression of Staphylococcal virulence genes. The method comprises contacting a candidate inhibitor with a SarA binding site of the agr (accessory gene regulator) locus in solution and assessing the binding of the candidate inhibitor to the SarA binding site of the agr locus. The identified inhibitors are useful for preventing and treating staphylococcal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP31524 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis lifection.
                                                                                                                                                                                                                                       1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                                                                                                                                        3 ISKINDCFELLAMVTYADRLKGIIKKEFSISFEEFAVLTYISENKEEEYYLKDIINHLNY 62
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5614.
specific binding sites of SarA protein on an accessory gene
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                                                                                                                                                                                         24.9%; Score 143; DB 22; 29.2%; Pred. No. 1.7e-06; ive 25; Mismatches 55;
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                                   Disclosure; Page 13; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                         ABP40769 standard; Protein; 148 AA
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97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis; antibacterial; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
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                                                                                                                                                                                       Query Match
Best Local Similarity 29.2<sup>3</sup>
Matches 33, Conservative
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08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermidis; open reading frame; ORF; bacterial infection; gene therapy.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                86
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                            1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI
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                                                                                                                                                                           Length 148;
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28.8%; Pred. No. 0.078;
iive 20; Mismatches 36;
                                                                                                                                                                        24.9%; Score 143; DB 23; 29.2%; Pred. No. 2.2e-06; ive 25; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 5018; 267pp; English.
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97US-064964P.
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Matches 23; Conserv
                                                                                                                    148 AA;
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Regulator of autolytic activity; RAT; autolysis; antimicrobial; antibacterial; screening; mutant; mutein.

Staphylococcus aureus.

WO200270666-A2.

12-SEP-2002.

06-MAR-2001; 2001US-273791P. 15-AUG-2001; 2001US-312546P. 12-OCT-2001; 2001US-329140P.

(DART-) DARTMOUTH COLLEGE

Cheung A;

06-MAR-2002; 2002WO-US06844

S. aureus regulator of autolytic activity (RAT) mutant protein.

08-JAN-2003

ABP54930;

ABP54930 standard; Protein; 134 AA.

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ABP54930
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               45 IFIL-HFTENHKEDLSLNMIIFYKNYQKNQLLKSITHLYEFNWISKKRHPYDQRRLVITL 103
                                                                                                                                                                                                              Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABD53124 to ABB3706. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent din or form part of the printed specification, but was obtained in electronic format directly from the
IYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVTV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VTELALDTGTVSPLLKRAMEQVDLIKAERSEVDQREVFIHLTDKSEM-IRPELSNASEKV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 5581; 267pp; English.
                                                                                                                        ABP40736 standard; Protein; 154 AA.
                                                         104 TQNQCSKITQLIDELEHFLE 123
                                            TDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                               98US-0134001.
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97US-064964P.
                                                                                                                                                                                                                         antibacterial; gene therapy
                                                                                                                                                                                                                                             Staphylococcus epidermidis.
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Les 30; Conserv
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                                                                                                                                                                                                                                                                                                               13-AUG-1998;
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                                                                                                                                              ABP40736;
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Matches
                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a mutant RAT (regulatory of autolytic activity) protein of Staphylococcus aureus. It is encoded by a mutant RAT gene (see ABV7308) identified in a Th551 transposon library of S. aureus strain RN6390. Transposon insertion results in a truncated RAT coding sequence, yielding a protein missing the last C-terminal 13 amino acids of the wild-type protein sequence (see ABV73629). A RAT mutant strain displayed significantly enhanced autolytic activity as compared with the parent. In the presence of penicilin, the RAT mutant showed increased lysis as compared with wild-type S. aureus. The invention provides RAT gene and RAT mutant miclaic acid sequences, the polypeptides encoded by these genes, vectors and sequences, the polypeptides encoded by these genes, or the polypeptides encoded by the mutant gene, or the polypeptides cutolytic activity of S. aureus and other bacteria through interaction with the RAT gene, RAT mutant gene, or the polypeptides concoded by them. These agents are expected to be useful in the inhibition of growth of S. aureus and other bacteria and in the treatment of bacterial infection, and can be used alone or in combination with an antibiotic such as penicillin to promote lysis of the bacteria. The RAT gene and gene products are also useful as research tools to enhance the understanding of the autolytic research tools to enhance the understanding of the autolytic research tools to enhance the understanding of the autolytic
                                                                                                      New regulator of autolytic activity (RAT) nucleic acid sequences and polypeptides, useful for regulating the autolytic activity of bacteria, inhibiting bacterial growth and infectivity, or for treating bacterial
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                                                                                                                                                                                                                                                                                                           Claim 7; Page 26; 26pp; English.
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Best Local Similarity 28.4%
Matches 25, Conservative
WPI; 2002-750455/81.
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                                        N-PSDB; ABV73908
                                                                                                                                                                                                                                     infection
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The present sequence is a novel regulatory of autolytic activity (RAI) protein of Staphylococcus aureus, which is involved in the control, modulation or regulation of autolytic activity. This the control, modulation or regulation of autolytic activity. This 17 kDa protein (predicted pl 7.38) is encoded by a novel gene (see ABV73907) that was identified in a Th51 transposon library of S. oureus strain RN6390 by screening for genes that affected expression of genes encoding the capsular polysaccharide of S. aureus. The invention provides RAI gene ARI mutant mucleic acid sequence, the polypeptides encoded by these genes, vectors and host cells, and a method of identifying agents that modulate the autolytic activity of S. aureus and other bacteria through interaction with the RAI gene, RAI mutant gene, or the polypeptides encoded by them: these agents are expected to be useful in the inhibition of growth of S. aureus and other bacteria and in the treatment of bacterial inflection. The RAI gene or gene products are also useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LVNATFQVKKFFRD-TXKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New regulator of autolytic activity (RAT) nucleic acid sequences and polypeptides, useful for regulating the autolytic activity of bacteria; inhibiting bacterial growth and infectivity, or for treating bacterial infection
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    The RAT gene or gene products are also useful as
tools to enhance the understanding of the autolytic

                                                               Staphylococcus aureus regulator of autolytic activity (RAT)
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16.3%; Score 93.5; DB 23;
Best Local Similarity 28.4%; Pred. No. 0.16;
Matches 25; Conservative 25; Mismatches 35;
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12-OCT-2001; 2001US-329140P.
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(first entry)
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                                                                                                                                                                 antibacterial; screening
                                                                                                                                                                                                                                   Staphylococcus aureus.
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N-PSDB; ABV73907.
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08-JAN-2003
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                                                                                                                                 Regulator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
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                                                                                                                                                                                                                                                                                                                                                                                                                             Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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   LKRMEQVDLIKRERSEVDQREVFIHLTD 100
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                                                                                                                                                                 ABB55470 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                     Lactococcus lactis protein zitR
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                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity
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Length 147;

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72

ABP54929 ID ABP5 XX AC ABP5 XX

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Antibacterial; gene therapy, vaccine, biosynthesis; biodegradation, vitamin B12; bacterial infection; disease.
    Listeria monocytogenes protein #1064.
                                                   11-APR-2001; 2001WO-FR01118.
                                                            11-APR-2000; 2000FR-0004629.
                         Listeria monocytogenes
                                                                    (INSP ) INST PASTEUR
                                 WO200177335-A2
                                          18-OCT-2001
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and blodegradation, especially biosynthesis of Vitamin BL2. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. Mote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.

The province of the print of the printed specification, but was obtained in electronic format directly from WIPO.

The province of the print of the printed specification, but was obtained in electronic format directly from WIPO.
Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, NG E, Varquez-Beland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charlic A, Durant L; Perez-Diac J, Baquero F, Garcia Del Portillo F, Gomez-Liopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID No 1065; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-010914/01.
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,, ,, 7 INDLVNATFQVKKFFRDTK-KKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYL 65 5; Gaps Query Match 16.1%; Score 92.5; DB 23; Length 141; Best Local Similarity 23.6%; Pred. No. 0.19; Matches 25; Conservative 30; Mismatches 46; Indels 5 ò

66 TKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEE 111

completed: November 17, 2003, 12:43:13 Search cor Job time

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us-10-043-539a-2.rai

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Sequence 4993, Ap Sequence 12, Appl Sequence 5151, Ap Sequence 5614, Ap Sequence 5618, Ap Sequence 5618, Ap Sequence 12, Appl Sequence 12, Appl Sequence 3734, Ap Sequence 4421, Ap Sequence 4421, Ap Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Appli Sequence 5609, Appli Sequence 5609, Appli Sequence 5609, Appli Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Sequence 5609, Ap Appli 5609, Ap Sequence 5609, Ap Appli 5609, Ap Sequence 5609, Ap Appli 5609, Ap Appli 5609, Ap Appli 5609, Ap Appli 5609, Ap Appli 5609, Appli 5609, Ap Appli 5609, Ap Appli 5609, Ap Appli 5609, Ap Appli 5609, Appli 5609, Ap Appli 5609, Ap Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, Appli 5609, 
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574
1 MSKINDINDLVNATFQVKKF.....DTQXANIQKLISELEEYIKN 115
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1. /GgTZ 6/ptodata/2/iaa/5A_COMB.pep:*

1. /GgTZ 6/ptodata/2/iaa/6A_COMB.pep:*

3. /GgTZ 6/ptodata/2/iaa/6A_COMB.pep:*

1. /GgTZ 6/ptodata/2/iaa/6B_COMB.pep:*

2. /GgTZ 6/ptodata/2/iaa/PGTUS_COMB.pep:*

3. /GgTZ 6/ptodata/2/iaa/PGTUS_COMB.pep:*

3. /GgTZ 6/ptodata/2/iaa/PGTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-676-722-12

US-09-134-01C-5151

US-09-134-01C-5151

US-09-134-001C-5614

US-09-134-001C-5614

US-09-134-001C-5618

US-09-134-001C-5618

US-09-134-001C-4980

US-09-134-001C-4980

US-09-134-001C-3734

US-09-134-001C-3734

US-09-134-001C-421

US-09-139-064-2

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US-09-134-001C-5609
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US-09-107-532A-7156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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US-09-723-262-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Sequence 2, Appli Sequence 512, Ap Sequence 5409, Ap Sequence 6403, Ap Sequence 629, Ap Sequence 28, Appli Sequence 28, Appl Sequence 28, Appl Sequence 28, Appli Sequence 4, Appli Sequence 10, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 644, Appli Sequence 6123, Ap Sequence 6124, Appli Sequence 6124, Appli Sequence 6124, Appli		SEQUENCES RELATING TO STAPHYLOCO AND THERAPEUTICS	Length 128; ; 0; Indels 0; Gaps 0;		IN L.L.P.
4 US-09-723-219-2 4 US-09-107-532A-651, 4 US-09-117-532A-640, 5 US-09-134-001C-540, 6 US-09-134-001C-525, 1 US-08-480-604A-28 2 US-08-134-01C-525, 1 US-08-480-604A-28 3 US-08-15-136-28 1 US-09-105-691-4 4 US-09-105-691-4 6 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-532A-5 4 US-09-107-6124	ALIGNMENTS .	D AMINO ACID R DIAGNOSTICS 34,001C ,964 is	<pre>\$; Score 486; DB 4; 8; Pred. No. 5.9e-44 8; Mismatches 1</pre>	FFRDTKKFNLNYEBIY FFRDTKKQYNLNYEBIX KKRSLQDERTVIVYYD	08676782 se ncent A. LATION OF EXOPROTEIN HYLOCOCCUS AUREUS E, SWECKER & MATHIS,
7.6 13.2 13.8 8 7.4 12.9 5.74 12.9 5.74 12.9 5.74 12.9 5.74 12.9 5.74 12.9 6.73 12.7 12.9 6.73 12.5 893 12.7 12.5 893 12.5 893 12.5 893		RESULT 1  US-09-134-001C-4993 Sequence 4993, Application US/091340) Sequence 4993, Application US/091340) GENERAL INFORMATION TITLE NOT INFORMATION: TITLE OF INVERTION: TITLE OF INVERTION: TITLE OF INVERTION: CURRENT APPLICATION NUMBER: US/09/12 CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064 PRIOR FILING DATE: 1997-08-14 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674 TYPER PROFILED NOS: 5674 TYPER PROFILED NOS: 5674 TYPER PROFILED NOS: 5674 CORGANISM: Staphylococcus epidermid. US-09-134-001C-4993	ch 1 Similarity 84.2° 96; Conservative	1 MSKINDINDLWNATFOVKK 15 MGKIKDINDLWNATFOVKK 15 MCKIKDINDLWNATFOVKK 61 KPYXLTKALQKLKDLKLLS 75 KPYXLTKALQKLKDLLS 75 KPYXLTKALQKLKDLNLLS	ESULT 2  Sequence 12, Application US/08  Patent No. 5976792  GENERAL INFORMATION: APPLICANT: CHEUNO: APPLICANT: FISCHETT!, Vinc TITLE OF INVENTION: REGULA TITLE OF INVENTION: REGULA TITLE OF INVENTION: TAPHY NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, STREET: P.O. BOX 1404  CITY: Alexandria
22888888888844444 800112848888888444444 		RESULT 1 US-09-134-00 Sequence 4 Fatent No.	Query Match Best Local Matches	À A À A	RESULT 2 US-08-675-76 Sequence ) Patent No GENERAL ) APPLICS A

Virginia

STATE:

occus

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; Score 146; DB 2;
; Pred. No. 3e-08;
27; Mismatches 51
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                REGISTRATION NUMBER: 39,300
REGISTRATION NUMBER: 0169
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR EAQ IN NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.4%;
29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Conservative
                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-676-782-13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  linear
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Matches 33; Conserv
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; ORGANISM: Staph
US-09-134-001C-5151
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US-09-134-001C-5614
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                                                                             COMPUTER: FLORDY disk
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,782
FILING DATE: US-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: MGGOWAN, MAICOLM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
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APPLICANT: CHEUNG, Ambrose
APPLICANT: CHEUNG, Ambrose
TITLE OF INVENTION: REQULATION OF EXOPROTEIN IN
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 15.782 FILING DATE: .08-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,505
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
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ZIP: 22313-1404
COMPUTER READBALE FORM:
COMPUTER: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08676782
Patent No. 5976792
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United States
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                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-676-782-13
COUNTRY:
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Sequence 5151, Application US/09134001C

Beach No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DATE: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14-14
RECORD FOR THE SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUE
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Patent No. 6380370

GENERAL INFORMATION:

TITLE OF INVENTION: DOUGETE-Stamm et al

TITLE OF INVENTION: BEIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C
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                                                                                                                          1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
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      Gaps
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      ·,
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      51; Indels
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15-05-134-001C-4980
Sequence 4980, Application US/09134001C
Patent No. 6.380370
GENERAL INFORMATION:
APPLICAMY: LUND DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8073, Application US/09328352
Patent NO. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT PILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8073
                                                                                                                                                                                                                                                                                                                                                                 8 MSEQHNIKEQLCFSLYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PVNVKKV·65
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.2%; Pred. No. 0.012;
Matches 30; Conservative 34; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.8%; Score 90.5; DB 4;
Best Local Similarity 27.1%; Pred. No. 0.03;
Matches 26; Conservative 25; Mismatches 42;
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     PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5581
LENGTH: 154
TYPE: PRT
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ORGANISM: Staphylococcus epidermidis
                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-5581
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US-09-328-352-8073
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Refear No. 6380370

GRNERAL INFORMATION:

APPLICANT: LAND DOUGETE-Stamm et al

APPLICANT: LAND DOUGETE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: REPERENCE: GT-C-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR PAPLICATION NUMBER: US 60/065,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5018

LENGTH: 249
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Petent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BEDERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERSIVE: 1998-08-13
CURRENT FILE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                      1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                     24.9%; Score 143; DB 4; Length 148; 29.2%; Pred. No. 8.9e-08; Live 25; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Mismatches
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 148
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5018
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.2%
Matches 33; Conservative
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Best Local Similarity 28.8<sup>§</sup>
Matches 23; Conservative
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US-09-134-001C-5581
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RESULT 13
US-09-107-532A-6399
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                                                                                                                           16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTK----ALQK 71
                                                                                                                                                    |:| :: | :: | :: | :: | 37 QLKHWLKIT---YRISIESEVULYKVY--ADTKISGKELRDTLHFEMLWDTSKIDVIIRK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 LRSESNEISSKEIA----KCSEPKPYY----LIKALQKLKDLKLLSKKRSLQDERTV 90
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د
                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08393985
Patent No. 5693476
GENERAL INFORMATION:
APPLICANT: Scheller, Richard H.
TITLE OF INVENTION: Methods and Compositions for Modulation
TITLE OF INVENTION: of Vesicular Release
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                      15.4%; Score 88.5; DB 4; Length 136; 27.3%; Pred. No. 0.043; ive 21; Mismatches 42; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 301;
                                                                                                                                                                                                            LKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELE 110
                                                                                                                                                                                                                                                IYKKELISKLESETDERQVYYFFDAKQKKLLDKMTGEIE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.7%; Score 84.5; DE
Best Local Similarity 26.1%; Pred. No. 0.32;
Matches 23; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
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US-09-252-991A-26170
; Sequence 26170, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SHOLTS. Charles K.
REGISTRATION NUMBER: 39,615
REFERENCE/DOCKET NUMBER: 8600-
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 301_amino_acids
                                                            Best Local Similarity 27.3
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein US-08-393-985-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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US-09-134-001C-4980
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US-08-393-985-12
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                                          Query Match
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US-09-134-001C-3734

) Sequence 3734, Application US/09134001C

) Sequence 3734, Application US/09134001C

) Patent No. 6380370

) GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: LYNN NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

) TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

) FILE REFERENCE: GTC-007
Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6399, Application US/09107532A
Patent No. 6583275
GENBRAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
14.6%; Score 84; DB 4; Length 368;
Best Local Similarity 28.6%; Pred. No. 0.46;
Matches 26; Conservative 23; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 OKLKDLKLLSKKRSLQDERTVIVYVTDTOKA 100
                              TITLE OF INVENTION: AUGUEIC ACID AND AMINO AC TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTIC FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 26170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 1998-08-13, PRIOR APPLICATION NUMBER: US 60/064,964, PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26170
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Best Local Similarity 24.0'
Matches 24; Conservative
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14.5%; Score 83; DB 4; Length 152;
Best Local Similarity 26.4%; Pred. No. 0.19;
Matches 32; Conservative 25; Mismatches 52; Indels
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Patent No. 642023

GENERAL INFORMATION:
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Barr, Philip
APPLICANT: Barr, Philip
APPLICANT: Falcipon BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUW TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
SOFTWARE: ASCII
APPLICATION UNDER: US/09/107,532A
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,51
ATTORNEY/AGENT INFORMATION:
NAME: ATTING DATE: J197
ATTORNEY/AGENT INFORMATION:
NAME: ATTING DATE: J0197
ATTORNEY/AGENT INFORMATION:
TELEBCOMMUNICATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELEBCOMMUNICATION INFORMATION:
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TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
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; LOCATION: (B) LOCATION 1...152
; SEQUENCE DESCRIPTION: SEQ ID NO: 6399:
US-09-107-532A-6399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 152 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 63999:
SEQUENCE CHARACTERISTICS:
                                                                                                                    STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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122 S 122
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RESULT 15
US-09-134-001C-4421
US-09-134-001C-4421
Patent No. 6380370
Patent No. 6380370
GENERAL INFORMATION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: UNCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/064,964
PRIOR PLILOR DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 NENDILNSRLKKRKYFLDVLESDLMQFKHISSNEYIIEDSFKLLNSEQKNILLKSYKYIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 ESVENDÍKFAQEGISÝÝ-EKVLAKÝKĎ-DLESÍKKVIKEÉKEKFPSSPPTTPPSPAKŤĎE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 ----EIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVI------VYVTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 DINDLVNATFQVKKFFRDTKKKFNLNYEEI----YILN---HILRSESNEISSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
FILING DATE: 14-FEB-1994
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 OK-----ANIO----KLISELEFYIKN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Davis Hoxie Faithfull Hapgood STREET: 45 Rockefeller Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.0%; Score 80.5; Di
Best Local Similarity 23.8%; Pred. No. 1.2;
Matches 36; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4421
LENGTH: 180
TYPE: PET
ORGANISM: Staphylococcus epidermidis
                                                                                                                 ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Plasmodium falciparum
STRAIN: MAD
                                                                                                                                                                                                                                                                                                                             LENGTH: 394 amino acids
TYBE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                         USA
                                                                                                         COUNTRY:
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us-10-043-539a-2.rai

US-09-134-001C-4421

8 NDLVNATFQVKK----FFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPY 63 Query Match 13.9%; Score 79.5; DB 4; Length 180; Best Local Similarity 19.3%; Pred. No. 0.55; Matches 26; Conservative 29; Mismatches 51; Indels 29; Gaps 101 NIQKLISELEEYIKN 115 ::: | | | : : | : 162 EMKYVFEELEQTIKH 176 g QQ ò Dp  $\delta$ ò

Search completed: November 17, 2003, 12:45:36 Job time: 23 secs

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Sequence 26,
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1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELBEYIKN 115
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUBL.pep:*

3: /cgn2_6/ptodata/2/pubpaa/NEG_NBW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666188 segs, 182559486 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 9, Assequence 3, Assequence 8, Assequence 4, Assequence 2, Assequence 2, Assequence 28, Sequence Sequence Sequence Sequence US-10-043-539-2 US-10-043-539-2 US-10-043-539-3 US-10-290-142-9 US-10-290-143-8 US-10-043-539-2 US-10-043-539-2 US-10-092-264-4 US-10-092-264-4 US-10-092-264-4 US-10-092-264-2 US-10-092-264-2 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-4 US-10-290-142-8 

Sequence 2 Sequence 3 Sequence 8

equence 7,	quence 5,	equence 4,	quence 11	ence 10	equence 6,	equence 5,		equence 76	equence 35	equence 76	equence 2,	equence 68	equence 5,	equence 5,	equence 2,	equence 4,	equence 7,	equence 7,	equence 3,	'n	equence 3, Appl	equence 2,	equence 18, App	equence 14, App	equence 16, App	equence 2,	equence 2,	equence 1,	a)
-10-290-143-	-10-290-14	-10-290-14	-10-156-761-	-10-087-464-10	-10-290-142-	-10-290-143-	62-	-10-032-585-76	-09-820-843A-	-10-032-585-76	-09-932-183A-	-09-738-626-6	-10-057-53	-10-057-532A-	-10-098-514-	-10-098-514-	-10-057-531A	-10-057-532A-	-10-057-531A	-10-057-532A-	-03-978-756-	-10-062-809-	-10-062-809-1	-10-098-51	-10-062-809-1	-10-057-531A-	-10-057-532A-	-10-057-531A-	-10-057-532A-
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Sequence 2, Application US/10043539;
Publication No. US20030114650A1
GENERAL INFORMATION:
Publication No. US20030114650A1
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
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APPLICANT: Cheung, Adar
APPLICANT: Cheung, Adar
APPLICANT: Cheung, Adar
APPLICANT: Cheung, Adar
APPLICANT: Cheung, Adar
APPLICANT: Cheung, Adar
APPLICANT: Cohorogyi
TITLE,OP INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
FILE REPREMENT: DC-01-01
PRIOR PELING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR APPLICATION NUMBER: US 60/289,601
PRIOR APPLICATION NUMBER: US 60/289,601
PRIOR PILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOTHWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 115
TWO 2
LENGTH: 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 115;
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100.0%; Score 574; DB 15;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , TYPE: PRT
, ORGANISM: Staphylococcus aureus
US-10-043-539-2
US-10-043-539-2
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1 MSKINDINDLVMATFQVKKFFRDTKKKFNLNYBEIYILNHILRSESNEISSKEIAKCSEF
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LOCATION: (114)...(114)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: MISC_FEATURE

) LOCATION: (120)...(120)

) OTHER INFORMATION: "X" is defined as any amino acid residue.

US-10-043-539-26
                                                                                                                                                                                                                                                                                   FEATURE:
AME/KEY: MISC FEATURE
ACALICON: (77) (78)
THER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                          URE: MISC_FEATURE
/KEY: MISC_FEATURE
TION: (86)..(87)
R INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE
LOCATION: (102)..(102)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAWE/KEY: MISC FEATURE
LOCATION: (1067)..(106)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE
LOCATION: (1177..(118)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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DTHER INPORMATION: "X" is defined as any amino acid residue.
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THER INFORMATION: "X" is defined as any amino acid residue.
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LOCATION: (110)..(110)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                         LOCATION: (58)...(59)
OTHER INFORMATION: "X" is defined as any amino acid residue
                                                                                                                             ION: (61)..(61)
INFORMATION: "X" is defined as any amino acid residue
                                                                                                                                                                                                                                 ION: (73)...(73): Is defined as any amino acid residue
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DIHER INFORMATION: "X" is defined as any amino acid residue
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Best Local Similarity 43.9%; Pred. No. 4.8e-15;
Matches 50; Conservative 15; Mismatches 49;
                                                                     FEATURE:
NAME/KEY: MISC FEATURE
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NAME/KEY: MISC_FEATURE
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NAME/KEY: MISC_FEATURE
NAME/KEY: MISC_FEATURE
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US-10-290-142-9
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                                                                        Sequence 26, Application US/10043539
Publication No. US20030114650A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Chang, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: DC-0199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (51)..(52)
OTHER INFORMATION: "X" is defined as any amino acid residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (2) ... (2) OTHER INFORMATION: "X" is defined as any amino acid residue. FEATURE:
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JCCATION: (4)...(4)
DTHER INFORMATION: "X" is defined as any amino acid residue.
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ION: (19)...(20
INFORMATION: "X" is defined as any amino acid residue.
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INFORMATION: "X" is defined as any amino acid residue.
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INFORMATION: "X" is defined as any amino acid residue.
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THER INFORMATION: "X" is defined as any amino acid residue.
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LOCATION: (10)...(10)
THER INFORMATION: "X" is defined as any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION: (15)..(17)
INFORMATION: "X" is defined as any amino acid
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AOCATION: (24)...(25)
THER INFORMATION: "X" is defined as any amino acid
FEATURE:
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,233
PRIOR PILING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-18
PRIOR PLING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 34
SOFTHING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 26
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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APPLICANT: Cheung, Ambrose
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AGENTS WHICH REGULATE AUTITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AGENTS WHICH REGULATE AUTITLE OF INVENTION: PROCESSES IN BACTERIA
FILE REFERENCE: DC-0202
CURRENT APPLICATION NUMBER: US/10/290,143
CURRENT APPLICATION NUMBER: US 10/092,264
PRIOR APPLICATION NUMBER: US 60/329,140
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-13-6
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-03-06
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8
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APPLICANT: McNamara, Peter
TITLE OF INVENTION: REQULATORS OF BACTERIAL VIRULENCE FACTOR EXPRESSION
FILE REFERENCE: KCC 4766
CURRENT APPLICATION NUMBER: US/10/145,602
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/291,917
PRIOR PILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYYTDTQKANIQKLISELEEYI 113
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              61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.8%; Score 148; DB 1930.1%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Mismatches
                                                                                                                                                                                            Sequence 8, Application US/10290143
Publication No. US20030124597A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-145-602-4; Sequence 4, Application US/10145602; Publication No. US20030171563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Staphylococcus aureus US-10-290-143-8
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ORGANISM: Staphylococcus aureus
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Best Local Similarity
Matches 30; Conserv
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Sequence 9, Application US/10290142

Publication No. US20030100002A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE

CURRENT APPLICATION NUMBER: US/10/290,142

CURRENT FILING DATE: 2002-03-06

PRIOR FILING DATE: 2002-03-06

PRIOR APPLICATION NUMBER: US 60/329,140

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/312,546

PRIOR APPLICATION NUMBER: US 60/312,546

PRIOR FILING DATE: 2001-09-15

PRIOR FILING DATE: 2001-09-15

PRIOR PRIOR FILING DATE: 2001-03-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Version 3.1

FENCIN. 194
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Publication No. US20030114650A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Chang, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
FILE REFERENCE: DC-0199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ITKINDCPELLSMVTYADKLKSLIKKEFSISFEEFAVLTYISENKEKEYYLKDIINHLNY 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 25.8%; Score 148; DB 15; Length 124; 1 Similarity 30.1%; Pred. No. 2e-07; 34; Conservative 27; Mismatches 52; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.8%; Score 148; DB 15; Length 124; 30.1%; Pred. No. 2e-07; ive 27; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,233
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/043,539 CURRENT FILING DATE: 2002-01-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-290-142-9
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Best Local Similarity
Matches 34; Conserv
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Best Local Similarity
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RESULT 9

US-10-04-539-27

Squence 27, Application US/10043539

Publication No. US20030114650A1

GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose

APPLICANT: Amana, Adar

APPLICANT: Amana, Adar

APPLICANT: Application SACTION

ITILE OF INVENTION: DACTERIA

FILE REFERENCE: DC-0199

CURRENT APPLICATION NUMBER: US/10/043,539

CURRENT PILING DATE: 2002-01-11

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR PLICATION NUMBER: US 60/261,607

PRIOR PLICATION NUMBER: US 60/261,607

PRIOR PLICATION OF 34

SOFTWARE: PARCENTIN VERSION 3.1

SERVICE FILING DATE: 2001-01-12

PRIOR PLICATION OF 34

SOFTWARE: PARCENTIN VERSION 3.1
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US-10-092-264-4
US-10-092-264-4

US-10-092-264-4

Sequence 4, Application US/10092264

Publication No. US2002064761A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BAC

TITLE OF INVENTION: 2002-03-06

CURRENT PELLOR DATE: 2002-03-06

PRIOR PILING DATE: 2002-03-06

PRIOR PLING DATE: 2001-03-06

PRIOR PLING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

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PRIOR FILING DATE: 2001-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                  69 QHIKVLVKHSYISKVRSKIDERNTYISISEEQREKIAERVTLFDQIIK 116
66 TKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 KALOKLKDLKLLSKKRSLODERTVIVYVTDTOKANIOKLISELEEYIK 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 16.6%; Score 95; DB 15; Length 119; 1 Similarity 21.3%; Pred. No. 0.038; 23; Conservative 29; Mismatches 56; Indels
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16.3%; Score 93.5; DB 14;
Best Local Similarity 28.4%; Pred. No. 0.062;
Matches 25; Conservative 25; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539-27
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; ORGANISM: Staphylococcus aureus
US-10-092-264-4
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Best Local Similarity
Matches 23; Conserv
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APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Cheung, Ambrose
APPLICANT: Annna, Adar
APPLICANT: Annna, Adar
APPLICANT: Cheung, Gongyi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
TITLE OF INVENTION: BACTERIA
FILLE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US 40/261,233
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 34
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Sequence 2, Application US/10145602
PUBlication No. US2030171563A1
GENERAL INFORMATION:
PUBLICATION:
PETER PEPERON:
FILE REFERENCE: KCC 476
CURRENT APPLICATION NUMBER: US/10/145,602
CURRENT FILING DATE: 2000-05-13
PRIOR APPLICATION NUMBER: US/201,917
PRIOR APPLICATION NUMBER: US/201,917
PRIOR APPLICATION NUMBER: US/201,917
PRIOR APPLICATION NUMBER: US/201,917
PRIOR PLING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 MKKVN--NDTVFGILQLETLLGDINSIFSEIESEYKMSREEILIL--LTLMQKGFMTLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSKINDINDLVNATFQ-----VKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKE
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                                     69 KNIKSLSKKGFINKSRNEADERRIFVSVTPIQRKKIACVINELDKIIK 116
KALOKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.9%; Score 120; DB 12; Length 166; 28.0%; Pred. No. 0.00018; tive 26; Mismatches 45; Indels 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 28, Application US/10043539; Publication No. US20030114650A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureus
US-10-145-602-2
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Best Local Similarity 28.0%
Matches 33; Conservative
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US-10-043-539-28
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LENGTH: 166
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Best Local S
Matches 27
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Sequence 2, Application US/10290142;
Publication No. US20030100002A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE ITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE ITLE OF INVENTION: METHODS FOR PRIOR PRIOR PRIOR PAPLICATION NUMBER: US/10/290,142
CURRENT APPLICATION NUMBER: US 10/092,264
PRIOR APPLICATION NUMBER: US 60/329,140
PRIOR PLING DATE: 2001-10-12
PRIOR PLING DATE: 2001-01-10-12
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-03-06
PRIOR PLING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: US 60/273,791
PRIOR PLING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 147
TWOEL DATE: DATE
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; Sequence 3, Application Wo. US20030124597A1
; Fublication No. US20030124597A1
; GENERAL INPORMATION:
; APPLICANT: Cheurg, Ambrose
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AGENTS WHICH REGULATE AUT:
; TITLE OF INVENTION: COMPOSITION BACTERIA
; FILE REFERENCE: DC-0202
; CURRENT APPLICATION NUMBER: US/10/290,143
; CURRENT APPLICATION NUMBER: US 10/092,264
; PRIOR PLING DATE: 2002-03-06
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2001-08-15
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                    15 LYNAQRQVNRYYSNKVFKKYNLTYPQFLVLT-ILWDES-PWNVKKVVTELALDTGTVSPL 72
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                                                                                                                             10 LVNATFOVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
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      Length 147;
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   16.3%; Score 93.5; DB 14;
llarity 28.4%; Pred, No. 0.069;
Conservative 25; Mismatches 35;
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16.3%; Score 93.5; DB 15;
Best Local Similarity 28.4%; Pred. No. 0.069;
Matches 25; Conservative 25; Mismatches 35;
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US-10-290-142-2
                             Best Local Similarity
Matches 25; Conserv
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US-10-290-143-3
      Query Match
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Publication No. US20020164761A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE REFERENCE: DC 108
FILE REFERENCE: DC 108
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 60/273,791
PRIOR APPLICATION NUMBER: US 60/273,791
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
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PRIOR FILING DATE: 2001-08-15
FUNDER OF EQ. ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.1
                                       LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
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; ORGANISM: Staphylococcus aureus
US-10-290-142-4
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; ORGANISM: Staphylococcus aureus
US-10-092-264-2
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Sequence 8, Application US/10290142

Publication No. US20030100002A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PREVENTING OR REDUCING MULTIPLE ANTIBIOTIC RESISTANCE
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: DC-0195
CURRENT FILING DATE: 2002-11-06
FRIOR APPLICATION NUMBER: US/10/290,142
PRIOR PILING DATE: 2002-03-06
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
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Best Local Similarity 28.4%; Pred. No. -0.069;
Matches 25; Conservative 25; Mismatches 35; Indels 3
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                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-290-143-3
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 147
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Search completed: November 17, 2003, 12:54:10 Job time: 267 secs

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OM protein - protein search, using sw model

Run on:

November 17, 2003, 12:36:25; Search time 25 Seconds (without alignments) 442.376 Million cell updates/sec

Title:

US-10-043-539A-2 574 1 MSKINDINDLVNATFQVKKF.....DTQKANIQKLISELBEYIKN 115 Perfect score:

Scoring table: Sequence:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	150	151	1388	150	144	338	964	1005	1875	154	155	260	755	1286	1639	1640
	14.6	14.6	14.6	14.5	14.4	14.4	14.4	14.4	14.4	14.3	14.3	14.2	14.2	14.2	14.2	14.2
	84	84	84	83	82.5	82.5	82.5	82.5	82.5	89	8	81.5	81.5	81.5	81.5	81.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

 B90028
 hypothetical protein sarR [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: B90028
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B90028
A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-115 <kur></kur>
 A; Cross-references: GB: BA000018; PID: 913702095; PIDN: BAB43387.1; GSPDB: GN00149
 A/Experimental source: strain N315
 C, Genetics:
 A;Gene: sarR
 100.08;
Best Local Similarity 100.0%; Pred. No. 7.36-40; Matches 115; Conservative 0; Mismatches 0; Indels 0; Gans 0;
QY 1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYBBIYLLNHILRSBSNBISSKBIAKCSEF 60
Db I MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEBIYILNHILRSBSNBISSKBIAKCSBF 60
Oy 61 KPYYLTRALOKLKDLKLLSKKRSLODERTVIVYVTDTOKANIOKLISELEEYIKN 115
-

# KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115 61 유

staphylococcal accessory regulator A [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001
C;Accession: B89831
R;Murcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A,Accession: B89831
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-124 «KUR»
A,Cross-references: GB:BA000018; PID:g13700508; PIDN:BAB41805.1; GSPDB:GN00149
A,Experimental source: strain N315

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Gaps

C,Genetics: A,Gene: sarA

à 연 ò 원

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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 22-Oct-2001
C;Accession: F90024
B;Kuroda, M.; Ohtea, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1.250 crUR>
A;Cross-references: GB:BA000018; PID:g13700028; PIDN:BAB41327.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics: A;Gene: sarH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:BA000018; PID:g13702067; PIDN:BAB43359.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; WUID:21311952; PMID:11418146
                                                7 INDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 DINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYL 65
                                                                                            9 VNKFINVEAYIFFLTQELKQQYKLSLKELLILAYFYYKNBHSISLKEIIGDILYKQSDVV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTK----ALQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 KALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                  66 TKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.0%; Score 115; DB 2; Length 250; 25.0%; Pred. No. 0.025; ive 26; Mismatches 55; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 101.5; DB 2;
illarity 29.3%; Pred. No. 0.13;
Conservative 23; Mismatches 38;
52;
Mismatches
  26;
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Best Local Similarity 25.0%
Matches 27; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: D89771
A,Status: preliminary
A,Molecule type: DNA
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A, Status: preliminary
A, Molecule type: DNA
     30;
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     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    "repressor of toxins Rot [imported] - Staphylococcus aureus (strain N315)
(.Species: Staphylococcus aureus
(.Species: Staphylococcus aureus
(.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
(.Accession: F89961 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
(.Accession: F89961 #sequence_revision 10. May-2001 #text_change 22-Oct-2001
(.A. Shiba, T.; Hatcri, N, Sobayashi, N, Sawano, T.; Thoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hatcri, N, Ogasawara, N, Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A889758; MUID:21311952; PMID:11418146
A;Accession: Pseliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
D90053
hypotherical protein sarH2 [imported] - Staphylococcus aureus (strain N315)
c,Species: Staphylococcus aureus
C,Species: Staphylococcus aureus
C,Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C,Accession: D90053
R,Kuroda, M:, Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Minutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 201
A,Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Cross-references: GB:BA000018; PID:g13702449; PIDN:BAB43590.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetical
A;Gene: sarH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-153 «KUR»
A;Cross-references: GB:BA000018; PID:g13701558; PIDN:BAB42851.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: rot
                                                                                                                                                                                                                                62
                                                                                                                                                                                  1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSKINDINDLVNATFQ-----VKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 MKKVN--NDTVFGILQLETLIGDINSIFSEIESEYKMSREBILIL--LTLWQKGSMTLKE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 IAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTD---TQKANIQKLISE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                  KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.4%; Score 123; DB 2; Length 153; 28.0%; Pred. No. 0.0033; ive 26; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 123; DB 2; Length 247; Pred. No. 0.0056;
                                                                              25.8%; Score 148; DB 2; Length 124; 30.1%; Pred. No. 2.5e-05;
                                                                                                                                  Indels
                                                                                                                               Mismatches
                                                                                                                            27;
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                                                                                                         30.1%;
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Best Local Similarity 28.05
Matches 33; Conservative
                                                                                                                               34; Conservative
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Best Local Similarity
                                                                                                         Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-247 <K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: D90053
A; Status: prelimina:
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                                                                                 Query Match
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à d ò Db.

ö

Gaps

'n

Gaps

71

m

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Zinc transport transcription regulator zitk [imported] - Lactococcus lactis subsp. lactic (Species: Lactococcus lactis subsp. lactis (Species: Lactococcus lactis subsp. lactis (C.)Species: Lactococcus lactis subsp. lactis (C.)Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 (C.)Accession: D86889 R.) Muncker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli A.; The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A; Reference number: A86625; MuID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: G89839

R;Kurcda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizamatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross references: GB.E005176; PID:g12725171; PIDN:AAK06214.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:BA000018; PID:g13700577; PIDN:BAB41874.1; GSPDB:GN00149
A;Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SA0641 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSLANQIDQFLGTIMQ----FAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 AKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVI------VYVTDTQKANIQKLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LVNATFQVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.3%; Score 93.5; DB 2;
Best Local Similarity 27.4%; Pred. No. 0.76;
Matches 34; Conservative 23; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
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llarity 28.4%; Pred. No. 0.77;
Conservative 25; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: transcription regulator yfiv
89 TVIVYVTDTQKANIQKLISELE 110
                               95 AVVLTITEKGNSVYEECEKQLE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 25; Conserv
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A Molecule type: DNA
A, Residues: 1-147 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-145 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 ELEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TYQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: D86889
A, Status: preliminary
A, Molecule type: DNA
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Cipercess Layout Mandoy Logenes
Cipercession: AEL198
KGlaser. P.; Frangeul. L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Ciporcession: AEL198
KGlaser. P.; Frangeul. L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Ciporces, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: ABI077; MUD:21537279; PMID:11679669
A.; Residues: L-141 < GLA>
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                                                                                                                                                                                                                 regulatory proteins (Mark family) homolog lmo0989 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n.
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16.4%; Score 94; DB 2; Length 150;
Best Local Similarity 24.4%; Pred. No. 0.72;
Matches 20; Conservative 27; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                         LKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Conservative
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Matches 26; Conserv
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Oguc K.;

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Dypothetical protein BB0512 - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Date: 0.3-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Date: 0.4-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Date: 0.4-Feb-1998 #sequence 0.4-Feb-1998 #text_change 08-Oct-1999

R;Fracer, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,

Som, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Atle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Accession: G70163

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DMA

A;Residues: 1-2166 <KLE>

A;Cross-;references: GB:AE001153; GB:AE000783; NID:g2688419; PIDN:AAC66876.1; PID:g2688426

A;Experimental source: strain B31
                                                                                                                                                                                                                                  Ritto, M.; Cooperberg, B.; Krulwich, T.A. submitted to the EMBL Data Library, February 1997
A; Description: Cloning and sequencing of Na+/H+ antiporter homolog gene from alkaliphilic A; Reference number: Z26111
A; Accession: T52550
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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C;Species: Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 T------KALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEBYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | | | : : | | : : | | : : | | : : | 31 KLEHNLTGEQFFVLNTL--EQKGRITSSQLABELQVKPSAITAMVDRLLKNDFVIRERDE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 KKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSL 84
                                                                                                                          C;Species: Bacillus firmus
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C;Accession: T52550
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                                                                                                probable transcription regulator 16.1K [imported] - Bacillus firmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-148 <1TO>
A;Cross-references: EMBL:099914; PIDN:AAB87745.1
A;Experimental source: strain OF4
C;Superfamily: transcription regulator yfiv
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15.8%; Score 90.5; DE
Best Local Similarity 26.5%; Pred. No. 1.4;
Matches 26; Conservative 24; Mismatches
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15.7%; Score 90; DB :
Best Local Similarity 32.2%; Pred. No. 27;
Matches 39; Conservative 18; Mismatches
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                                                                                                                                      ATPASE involved in DNA repair [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Bate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: G97236 C;Accession: G97236 C;Accession: G97236 C; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol: 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium (A;Reference number: A96900; MUID:21359325; PMID:21359325
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D90028

hypothetical protein [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Accession: D90028

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, i.; (C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001

C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Reference number: A89759, MUID:21311952; PMID:11418146

A;Status: preliminary

A;Status: preliminary

A;Status: DANA

A;Reference number: CRIMPA

A;Reference number: ARMA

A;Reference number: ARMA

A;Reference number: ARMA

A;Reference number: ARMA

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A;Acatus: preliminary
A;Molecule type: DNA
A;Residues: 1-1163 «KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80682.1; PID:g15025772; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Wolecule type: DNA-
;Residues: 1-247 «KUR»
;Cross-references: GB:BA000018; PID:g13702097; PIDN:BAB43389.1; GSPDB:GN00149
;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYYLTKALQKLKDLKLLSKK---RSLODERTVIVYVTDTQKANIQKLISE----LEEYIK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYVSYLLSSOELFRNIKCYLNMCQLTLEELYVLG-ILNLHKGQLTVKELQ--GBFHHPIF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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LKRMEQVDLIKRERSEVDQREVFIHLTD 100
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Matches 36, Conserv
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A; Experimental
C; Genetics:
A; Gene: SA2091
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Gaps

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Gaps

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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AC1556
R;Glaser, P. Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Do; Jones, L.M.; Karst, U. Science 294, 849-882, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Authors: AB1077; MUD:21537279; PMID:11679669
A;Accession: AC1556
A;Molecule type: DNA
A;Residues: 1-141 < GLA>
A;Coss-references: GB:AL52022; PIDN:CAC96219.1; PID:g16413447; GSPDB:GN00178
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:
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15.4%; Score 88.5; DB 2; Length 141;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 25; Conservative 26; Mismatches 48; Indels 1
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November 17, 2003, 11:25:47; Search time 15 Seconds (without alignments) 360.538 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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574 1 MSKINDINDLVNATFQVKKF.....DTQKANIQKLISELEEYIKN 115 Gapop 10.0 , Gapext 0.5 US-10-043-539A-2 **BLOSUM62** Title: Perfect score: Scoring table: Sequence:

127863 Total number of hits satisfying chosen parameters: 127863 segs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

esult No. Score	a)		Len	DB	SUMMAKIES	cri)	ion
         	93	. 9	1 40	-			clostridium
88	'n.	15.4	875	Н		P31111	Sch
85	•	4.	9	М		051578	borrelia bu
84		4.	0	Н	STX5_RAT	008851	rattus norv
83		4.	$^{\circ}$	٦		Q96dt5	homo sapien
82		4.	ω	٦	DPOL_CBEPV	P30319	choristoneu
82		4.	0	Н	RASO_METJA	058718	methanococc
82		•	87	٦	MLP1 YEAST		saccharomyc
81			φ	Н	DP3X_MYCGE		mycoplasma
81		4.	63	Н	MSP1_PLAFK		plasmodium
81		4.	m	Ч	MSP1_PLAFW		plasmodium
81		4.	34	-1	TPR HUMAN		homo sapien
	81	4.	4	Н	OHRR BACSU		bacillus su
4	81	4.	50	۳H	TRPE_HELPY	•	helicobacte
2	81	14.1	œ	Н	RPO1_VARV	~	variola vir
6 80		4	0	Н	ENGB_WIGBR	~	wiggleswort
7 80		•	0	Н	RUVB_MYCGE		mycoplasma
8 80		•	н	ч	YC09_CAMJE		campylobact
o.	80	•	S	Н	YDY3_SCHPO		schizosacch
0	æ	•	N	Н	MFD_BORBU	051568	borrelia bu
1 79		•	4	H	YPOP_BACSU	P54182	bacillus su
	79	•	9	Н	PRIA_BORBU	045032	borrelia bu
3	79	•	σ	٦	BXA2_CLOBO	Q45894	clostridium
4	79	•	79	Н	USO1_YEAST	P25386	saccharomyc
5 78	٠		7	Н	XISA_ANASP	P08862	anabaena sp
6 78			w	Н	APG6 YEAST	002948	saccharomyc
7	78	•	N	Н		Q8k987	buchnera ap
8 77		•	S	Н	BN11_YEAST	P41832	aromy
6	11	m.	7	Н		Q9v785	drosophila
16	•	т	α	Н	RASO PYRFU	P58301	pyrococcus
76			90	Н	YCF0 MARPO	P12221	marchantia
76	•	س	æ	7	RPO1 VACCC	P20504	vaccinia vi
76	•	Э.	28	Н	RPO1_VACCV	P07392	vaccinia vi

P13819 plasmodium P08569 plasmodium		002224 homo sapien 067642 aquifex aeo		Q59037 methanococc P19598 plasmodium	P52611 borrelia bu Q8d2w8 wiggleswort
MSP1_PLAFF MSP1_PLAFM	MSP1_PLAFC MSP1_PLAFP	CENE HUMAN TKT AQUAE	SCPI MESAU SCP1 MOUSE	SMC METJA MSPI PLAF3	FLIH_BORBU SYA_WIGBR
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13.3	13.3 13.3	13.3	13.2	13.2	13.2
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3.4	37	3 3 3	4.4.0 0.1	4, 4, 5, 6,	4 4 5 4

### ALIGNMENTS

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STRAIN=ATCC 824 'A'.

X MEDLINE=21359325; PubMed=11466286;

A Noelling J. Breton G., Omelbenko M.V., Makarova K.S., Zeng Q.,

A Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

"Genome sequence and comparative analysis of the solvent-producing

"Genome sequence and comparative analysis of the solvent-producing

"J Bacteriol 183:4823-4838(2001)

"J Bacteriol 183:4823-4838(2001)

"J Bacteriol 183:4823-4838(2001)

"C in FUNCTION: Sbocco leaves DNA hairpin structures. These structures

recombination reactions. The complex acts as a 3'->5' double

strand exonuclease that can open hairpins. It also has a 5'

single-strand endonuclease activity (By similarity).

- SUBDNIT: Heterodimer of sboc and sbob (By similarity).

- SIMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Absurvi, 29, 236.

PIR; G97236, G97236.

InterPro; IPR003439; ABC transporter.

Hydrolase; Nuclease; Exchuclease; Endonuclease; DNA replication; Hydrolase; Nuclease; Exchuclease; Colled coil; Complete proteome. NP BIND 35 COLED COIL (POTENTIAL).

DOMAIN 197 415 COILED COIL (POTENTIAL).

DOMAIN 446 1003 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SBCCase SaccD subunit C.
SBCC OR CAC2736.
    PRT; 1163 AA.
STANDARD;
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Query Match
16.2%; Score 93; DB 1; Length 1163;
Best Local Similarity 29.8%; Pred. No. 4.2;
Matches 36; Conservative 18; Mismatches 39; Indels 28; Gaps

3 KINDINDLVNATFQVKKFFRDTKKKFN-LNYEEIYILNHILRSESNEISSKEIAKCSEFK 61

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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., A Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., A Johnston M., Andrews S., Brinkman R., Gorco T., Kirsten J.,

Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,

A Mardis E., Menezes S., Miller N., Nan M., Pauley A., Peluso D.,

A Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,

A Rifken L., Rohldman P., Vaudin M., Wilson R., Waterston R.;

Submitted (MAR.1996) to the EMBL/GenBank/DBJ derabases.

I. Submitted (MAR.1996) FOR MILOTIC CHROMOSOME SYMAPSIS AND CELL CYCLE PROGRESSION. MAY ACT AS A MOLECULAR ZIPPER TO BRING HOWOLOGOUS CHANGONGENES IN CLOSE APPOSITION. ZIPPER TO BRING HOWOLOGOUS CHANGONGONES IN CLOSE APPOSITION. ZIPPER TO BRING HOWOLOGOUS CHANGONGONES.
                                                   873 KVNDI-DKLNKILMEEKFENIEKAKENYLNDKEINLLKSDVEKYKNELSKVNGA----- 925
                                PYYLTKALQKLKDLKLLSKK---RSLQDERTVIVYVTDTQKANIQKLISE----LEEYIK 114
                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sym M., Engebrecht J.A., Roeder G.S.; "ZIP1 is a synaptonemal complex protein required for meiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0 30.002073, 2.5ynaptonemal complex; IDA.
GO; GO:0007126; P:melosis; IMP.
GO; GO:0007129; P:synapsis; IMP.
GO; GO:0007129; P:synapsis; IMP.
Nuclear protein; Melosis; Coiled coil.
DOMAIN 177 333 COILED COIL (POTENTIAL).
DOMAIN 397 438 COILED COIL (POTENTIAL).
CONFLICT 55 55 T -> A (IN REF. 1).
SEQUENCE 875 AA; 100035 MM; 674F12625CD9DDFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                           (Rel. 34, Last sequence update)
(Rel. 36, Last annotation update)
complex protein ZIPI.
                                                                                                                                                                                                                       875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88.5;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BR1824-3B;
MEDLINE=93161412; PubMed=7916652;
                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 106487, AAA35239.1; -. EMBL, U51031, AAB6474.1; -. PIR, S70115, S70115. SGD; S0002693; ZIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.4%;
                                                                                                                                                                                                                                                                                                                              OR YDR285W OR D9819.9
                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72:365-378(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome synapsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=4932;
                                                                                                                                   973
                                                                                                    115 N 115
                                                                                                                                                                                                                                                                                                               Synaptonemal
                                                                                                                                                                                                                                                        01-JUL-1993
                                                                                                                                                                                                                                                                            01-OCT-1996
                                                                                                                                                                                                                                                                                           15-JUL-1998
                                                                                                                                                                                                                      ZIP1 YEAST
                                                                                                                                   973 N
                               62
                                                                 926
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                                                                                                                                                                                                       ZIP1_YEAST
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Best Local Similarity

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  4
                                                                                677
                                                                                                                                                    8 NDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98065943; PubMed=9403685;
KEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00580; UvrD-helicase; 1.
TICRFAMS; TIGR00609; recB; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
                                                                                621 NEOKDHTTKLEAFOKNNEOLOKLNVEVVOLKAHELELEE---ONRHLKNCLEKKETGVEE
                                                                                                                         68 ALQKLKDLK------LLSKKRSLQDERTVIVYVT-----DTQKANIQKLISE
23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'-or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burgdorferi.";
Nature 390:580-586(1997)
-!- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE
UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-
STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.
ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. UVRD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphooligonucleotides.
SUBUNIT: CONSIST OF THREE SUBUNITS, RECB, RECC AND RECD
  Indels
  46;
                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2000 (Rel. 39, Last sequence update)
Exodeoxyribonuclease V beta chain (EC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA repair, Complete proteome.
NP BIND 18 25 ATP (POTENTIAL).
  26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P56255; 1PJR.
1218, BB0633; -.
InterPro; 1PR004586; RecB.
InterPro; 1PR000212; UvrD-helicase.
                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001164; AAC66981.1; -. PIR; H70178; H70178.
  Conservative
                                                                                                                                                                                                              109 LEEYIKN 115
                                                                                                                                                                                                                                                       738 LEE-IKN 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=139;
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DB 1;

us-10-043-539a-2.rsp

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Query Match
Best Local Similarity
                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                   DNAH11
                                                                                        원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                296 DNRNKNR-----NNLKQYVILKVEYKILKYIEKELKKTIKSTNTIDQNYIISNLKNYLKS 350
                                                                                                                   237 SKENDIFKIAE-TLIKNKFFSTLIEKETKKNSKLSPKELKIKNDLICLGINIKHEKYKSE 295
                                                                                                                                                46 SNEISSKEIAKCSEFKPYYLTKALQKL-----KDLKLLSKKRSLQDERTVIVYVTDTQKA 100
                                                                                            45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SKINDINDLVNATFQVKKFF-----RDTKKKFNLNYEEIYILNHIL------RSE
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SYXXA OK SIXXS.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
ANCHOR FOR TYPE IV MEMBRANE PROTEIN
                                                                  27;
                                       DB 1; Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FOTENTIAL).
VESICULAR (POTENTIAL).
COLLED COIL (POTENTIAL).
T-SNARE COLLED-COIL MOCLOGY.
F-SGOALA079C8A9F7 CRC64;
                                                                  Indels
           B61D63C1C959B91F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fransport; Golgi stack
                                                                  48;
                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                     Query Match 14.9%; Score 85.5; DB Best Local Similarity 24.6%; Pred. No. 16; Matches 33; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                 301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, F48213; F48213.
InterPro; IPRO06012; Syntaxin.
InterPro; IPRO06011; Syntaxin.N.
InterPro; IPRO06011; Syntaxin.N.
Pfam; PF00804; Syntaxin; 1.
SMART; SMO0397; T. SNARE; 1.
PROSITE; PS00914; SYNTAXIN; 1.
PROSITE; PS00914; SYNTAXIN; 1.
           137828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34117 MW;
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DOMAIN 1 279
TRANSMEM 280 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L20822; AAA03047.1; -.
                                                                                                                                                                                                     101 NIOKLISELEEYIK 114
                                                                                                                                                                                                                       351 EDKKLINAIKURYK 364
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
           1169 AA;
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209
301 AA;
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DOMAIN
SEQUENCE
           SEQUENCE
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STX5_RAT
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92
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-!-SUBDOXII: Consists of at least two heavy chains and a number of intermediate and light chains.
-!-DOMAIN: Dynain heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynain components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring, A stalk-like structure (formed by two of the coiled coil domains) protrides between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPsae sites, one per AAA domain. Probably only one of these (within AAA)
                                                                                                                            42 LRSESNEISSKEIA----KCSEFKPYY-----LTKALQKLKDLKLLSKKRSLQDERTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Force generating protein of respiratory cilia. Produces force towards the minus ends of microtubules. Dynein has APPase activity, the force-producing power stroke is thought to occur on release of ADP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (ICS1), also known as primary ciliary dyskinesia (PCD). The phenotype of this autosomal recessive disease is characterized by axonemal abnormalities of respiratory cilia and sperm tails leading to bronchiectasis and sinusitis, which are sometimes associated with situs inversus (Kartagener syndrome) and male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34;
SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34;
VAL-3715; PRO-3765 AND ILE-4177.
TISSUE-Nasal epithelium, and Testis;
MEDLINE=22155903; PubMed=1214444;
MEDLINE=22155903; PubMed=1214444;
Bartoloni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N. Rossier C., Jorissen M., Armengot M., Meeks M., Mitchison H.M., Change E.M., Delozier-Blanchet C.D., Craagen W.J., Antonarakis S.E.;
"Mutations in the DNAHII (axonean heavy chain dynein type 11) gene cause one form of situs inversus totalis and most likely primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: Defects in DNAH11 are a cause of immotile cilia syndrome
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                               Q96DT5; Q9UJ82;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
L5-SEP-2003 (Rel. 42, Last annotation update)
Ciliary dynein heavy chain 11 (Αχοπεπα1 beta dynein heavy chain 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              actually hydrolyzes ATP, the others may serve a regulatory
                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Nasal polyps; Matti A.K., Mattei M.-G., Jorissen M., Volz A., Ziegler A., Bouvagnet P.; educater P., educater P., education of human dynein heavy chain genes. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sterility. -- SIMILARITY: Belongs to the dynein heavy chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ciliary dyskinesia.";
Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286(2002)
                                                27;
; Score 84.5; DE; DE; Pred. No. 4.6; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                             4523 AA
                                                                                                                                                                                           91 ----IVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                                                                                                                      EIEELTYIIKODINSLNKOIAQLQDFVR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1904-2004 FROM N.A. TISSUE=Nasal polyps;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                             InterPro; IPR003593; AAA ATPase.
InterPro; IPR005613; AIP3.
InterPro; IPR004273; Dynein_heavy.
Pfam; PF03028; Dynein heavy; I.
SMART; SM00382; AAA; 4.
Motor procein; Dynein; Microtubules; ATP-binding; Repeat; Coiled coil;
DoMAIN 1 1sease mutation.
SYEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROVEN TO BE
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AAA 2 (BY SIMILARITY).
AAA 3 (BY SIMILARITY).
AAA 4 (BY SIMILARITY).
AAA 5 (BY SIMILARITY).
AAA 5 (BY SIMILARITY).
AAA 6 (BY SIMILARITY).
AAA 6 (BY SIMILARITY).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VAR 013858.
                                                                                                                                                                                                                                                                                                                                                                                                                                / -> A.
'FTId=VAR_013854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --> V.
/FTId=VAR_013861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    rTId=VAR_013855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> T.
FTId=VAR_013860.
                                                                                                                                                                                                                                                                                                                                                                                         ) -> R.
/FTId=VAR_013852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) -> G.
'FTId=VAR_013856.
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/FTId=VAR_013862
                                                                                                                                                                                                                                                                                                                                                                                                            -> C.
FTIG=VAR_013853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIId=VAR_013857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTId=VAR_013859
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ATP (POTENTIAL)
ATP (POTENTIAL)
ATP (POTENTIAL)
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SUBSTITUTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4523 AA; 520969 MW;
                                                                             EMBL, AJ320497; CAC60121.1; -. EMBL, AJ132087; CAA10560.1; -. Genew; HGNC:2942; DNAH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                     2373
2726
3073
3410
34129
4129
1327
3143
3410
1907
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2524
2869
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les 32; Conserv
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                                                                                                            MIM; 603339; -
                                                                                                                      MIM; 242650; -
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Matches
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7 INDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the ENBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   3108 NGIQKLKTTASQVGDLKARLASQEAELQLRNHDAEALITKIGLQTEKVSREKTIADAEE 3166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 -----KKKYIGEVVSSMNPLQLISDSKG-----TALIRRDCTEIHKTILKNTIDILK 862
67 KALQKLK-----DLK--LLSKKRSLQ----DERTVIVYV-TDTQKANIQKLISELEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SKINDINDLVNATFQVKKF----FRDTK-----KKFNLNYEEIYILNHILRSESNEISSK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92199242; PubMed=1840516;
Mustafa A., Yuen L.;
"Identification and sequencing of the Choristoneura biennis
entomopoxvirus DNA polymerase gene.";
DNA Seq. 2:39-45(1991).
-! - CATIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                01-APR.1993 (Rel. 25, Created)
01-APR.1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7).
Choristoneura biennis entomopoxvirus (CbEPV):
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirus B.
NCBL TAXID=10288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
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23.2%; Pred. No. 23;
tive 23; Mismatches
                                                                                                                                                                                                                                964 AA
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(Rel. 40, Last sequence update)
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PIR; S25855; S25855.
InterPro; IPR006172; DNA_DOL B.
InterPro; IPR006134; DNA_DOL B.
InterPro; IPR006133; DNA_DOL B.
Pfam; PF00136; DNA_DOL B. 1.
SNART; SM00486; POLES; 1.
PROSITE; PS00116; DNA_POLES; 1.
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ID RASO METJA
AC QS8718;
DT 16-OCT-2001 ()
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                                                                                                                                                                                                                                CBEPV
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DPOL_CBEPV
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ALL-I, DSM 2661 / ATCC 43067;
MDDLINE-96337999; Pubmed-8686887;
Bult C.J., White O., Olsen G.J., Zhou L., Fletschmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fletschmann R.D.,
Sutton G.G., Blake J.A., FitzZerald L.M., Clayron R.J., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Filtmann J.L.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 273:1058-1073(1996).
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KINDINDLVNATFQVKKFFRDTKKKFN-----LNYEBIYILNHILRSBSNBISSKBIAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Forms a complex with mre11 (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1005 AA; 119387 MW; 9BBBB48173E788F3 CRC64;
                                                                                                  Archaea, Euryarchaeota, Methanococci, Methanococcales,
Methanocaldococcaceae, Methanocaldococcus.
28-FEB-2003 (Rel. 41, Last annotation update)
DNA double-strand break repair rad50 ATPase.
ABD50 OR M11322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TICK, M01322; --
HAWAP; MF 00449; -: 1.
HAWAP; MF 00449; -: 1.
Interpro: IPR003439; AAA_ATPase.
Interpro: IPR003405; SMC_C.
Interpro: IPR003405; SMC_N.
Pfam; PF04423; SMC_O.
Pfam; PF04463; SMC_C; 1.
ProDom; PF00464; SMC_C; 1.
ProDom; PF00465; ABC transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U67572; AAB99331.1; -. PIR; A64465; A64465.
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                                                                                 Methanococcus jannaschii.
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Matches 35; Conserv
                                                                                                                                                            NCBI_TaxID=2190;
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1875 AA

PRT;

STANDARD;

RESULT 8 MLP1\_YEAST ID \_MLP1\_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 BEKRPYYLTKALOKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISE-LEEYIKN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 NDINDLVNATFQVKKFFRDTKKKF-----NLNYEEIYILNHILRSESNEISSKEIAKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-94205265; PubNed-8154186; Bou G., Esteban P.F., Baladron V., Gonzalez G.A., Cantilejo J.G., Remacha M., Jümenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; Remacha M., Jümenez A., del Rey F., Ballesta J.P.G., Revuelta J.L.; The complete sequence of a 15,820 bp segment of Saccharomyces cerevisiae chromosome XI contains the UBI2 and MPL1 genes and three new open reading frames."; Yeast 9:1149-1154(1993).
                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93247549; PubMed=8483450;
Koelling R., Nguyen T., Chen E.Y., Botstein D.;
"A new yeast gene with a myosin-like heptad repeat structure.";
Mol. Genet. 237:359-369(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 82.5; DB 1; Length 1875; 28.8%; Pred. No. 47; ive 23; Mismatches 50; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R -> A (IN REF. 1).
MW; 683A0D34C9066867 CRC64;
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
R -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: SOME, TO THE TPR ONCOGENE.
-!- CAUTION: REF.2 MISQUOTES THE GENE NAME AS "MPL1".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005635; C:nuclear membrane; IDA.
GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0006606; P:protein-nucleus import; IDA.
COLEd coil; DNA repair. COLLED COLL (POTEN
01-OCT-1993 (Rel. 27, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
MLP1 OR YKR095W OR YKR415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
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(Rel. 33, Last sequencé update)
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EMBL, X73541, CAA1948.1;
EMBL, Z28320; CAA82174.1;
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Best Local Similarity 28.8
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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1875 AA;
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SGD; S0001803; MLP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                              STRAIN=S288C;
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P47659;
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01-FEB-1996
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ID DP3X_M
AC P47659
DT 01-FEB
DT 01-FEB
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RESULT 10
WSP1 PLAFK

ID WRSP1 PLAFK
AC P04932;
DT 13-AUG-1987 (Rel. 05, Created)
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PRT; 1630 AA

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CARBOHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 LFIFTTTEFNKIPLTILSRCQSFFFKKITSDLILERLND---IAKKEKIKIEKDALIKIA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                     SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a tau subunit. This core dimerizes to form the POLIII' complex. PolIII' associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).
                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R.; Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 -----NEISSKEIAKCSE--FKPYYLTKALQXLKDLKLLSKKRSLQDERTVIVYVT
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                                                          Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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SMART; SM00382; AAA; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
ATP-binding; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 51 ATP (POTENTIAL).
260 AA; 29772 MW; 80908B0FID6D78D4 CRC64;
 28-FEB-2003 (Rel. 41, Last annotation update) DNA polymerase III subunit gamma (EC 2.7.7.7) DNAX OR DNAH OR MG420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.2%; Score 81.5; DE 22.8%; Pred. No. 6.9; iive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR003593; AAA ATPAse.
INTERPRO; IPR003959; AAA ATPAse centr.
InterPro; IPR000862; RFCdomain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22.8% les 31, Conservative
                                              Mycoplasma genitalium.
                                                                          NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                            DNA (N)
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                                                             Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 INDINDLV------NATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTIGENS OF
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS, SEQUENCE FROM N.A.
BADAW, TOOLLE R., Bujard H.;
Submitted (JUW-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS O MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                 MEDLINE-86136024; PubMed=3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Katunenberg H., Bujard H.; Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; Iransmembrane; GPL-anchor.
SIGNAL
1 19 MEDOTATIAL.
CHAIN
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                                                                                             MSP-1. "Plasmodium falciparum (isolate Kl / Thailand).
Plasmodium falciparum (isolate Kl / Thailand).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADBDEC3CE0A46322 CRC64;
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22; Mismatches
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Pred. No. 49
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25.4%;
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1630
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                                                                                                                                                                       NCBI_TaxID=5839;
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1165
1436
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                                                                      (PMMSA) (P190)
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249 IENINELIEESKKTIDKNKNATKEEEK-----KKLYQAQY-DLSIYNKQLEEAHNLISVL 302
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=86014355; PubMed=2995820;
Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                      .(*Potencial).
-!- PTM: MERGOLIE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE NAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                       Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
                                                                                13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P195).
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                                                                                                                                                                                                                                                                                                "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A24594; A24594.
PIR; S05603, S05603.
InterPro; IPR006209; EGF_like.
Pfan, PF000008; EGF, I.
Malaria, Merzorie; Polyprotein; Repeat; Signal; Glycoprotein; Transmembrane; GPI-anchor; 3D-structure.
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Pred. No. 49;
                                                                                                                                                   Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5848;
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(GLCNAC...)
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Best Local Similarity 25.4
Matches 35; Conservative
                                                      STANDARD;
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P04933;
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MSP1 PLAFW
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DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html"
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                REVISIONS, AND CHARACTERIZATION.
MEDLINE=95096166; Publed=7798308;
Byrd D.A., Green D.J., Pante N., Cooper C.S., Aebi U., Garace L.;
Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
-----LLSKKRSLQDERTVIVYVTDTQK
                                                                                                                                                                                                                                                                                                                                                                          Mitchell P.J., Cooper C.S., "The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                  2349 AA
EIAKCSEFKPYYLTKALQKLKDLK-----
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                                                          100 ANIOKLIS---ELEEYIK 114
                                                                                       363 FNIDSLFTDPLELEYYLR 380
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                                                                                                                                                                  STANDARD;
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MIM; 189940; -.
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16 QVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDL 75
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WEDINID=98044033; PubMed=9384377;

KUNDEL F., Oggasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Burschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Brouillet S., Brington T., Pabret C., Ferrari B., Foulger D.,

A Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

A Brian K.D., Errington T., Fabret C., Ferrari B., Foulger D.,

A Fritz C., Fujita M., Pujita Y., Fuma S., Galieron N.,

A chisepii G., Guy B.J., Hage K., Halech J., Harwood C.R., Hennut A.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

A Milbert H., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
                                                                                                                                                                                                                                                                                                                                                            1468 EQHVSVQEMQELKETINQAETKSKSL------ESQVENLQKTLSEKETEARN 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devine K.M.; "Sequence of the Bacillus subtilis genome between xlyA and ykoR."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     DB 1; Length 2349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Organic hydroperoxide resistance transcriptional regulator.
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                               AFDD6885CEDCA9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
GO:0005643; C:nuclear pore; TAS.
GO:0006606; P:protein-nucleus import; TAS.
led coil; Proto-oncogene; Chromosomal translocation;
                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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2349 AA; 265600 MW;
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                                                                                                                                                                                                                                                     14.2%;
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GO, GO:0005643; C
GO; GO:0006606; P
Coiled coil; Prot
Nuclear protein;
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03477;
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Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Presecout A.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecout B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadale Y.,
A Sato T., Scanlar E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Secwska A., Sero S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi B., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Togarotti A.,
Vari A., Wambutt R., Vandenbol M., Vannier F., Vasasactti A.,
Vari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Minters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
subtilis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- FUND. Oxidation on Cys-15 in response to redox signaling leads to the loss of DNA-binding activity and the inactivation of repressor function. Oxidized OhrR can be further reduced by thiol reductants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSTEINE SULFENIC ACID (-SOH) (PROBABLE)
C-5G,S: FULL REPRESSOR ACTIVITY, BUT NO
MODULATION BY PEROXIDE.
+ 4F277EA9ABSEE861 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuangthong M., Atichartpongkul S., Mongkolsuk S., Helmann J.D., "OhrR is a repressor of ohrA, a key organic hydroperoxide resistance determinant in Bacillus subtilis."; J. Bacteriol. 183:4134-4141(2001).
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(14)

OXIDATION OF CYS-15, AND MUTAGENESIS OF CYS-15.

MEDLINE=22008016; PubMed=11983871;

Fuangthong M., Helmann J.D.;

"The ONTR repressor senses organic hydroperoxides by reversible formation of a cysteine-sulfenic acid derivative.";

Proc. Natl. Acad. Sci. U.S.A. 99:6690-6695(2002).

-!- FUNCTION: Organic peroxide sensor. Represses the expression peroxide-inducible gene ohra by cooperative binding to two inverted repeat elements.

-!- ENZYME REGULATION: Inactivated by oxidation of Cys-15 to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and repressor activity restored. SIMILARITY: BELONGS TO THE MARR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00347; HTH MARR; 1.
PROSITE; PS01117; HTH MARR FAMILY; FALSE_NEG.
DNA-binding; Transcription regulation; Repressor; Oxidation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21311737; PubMed=11418552;
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BMBL; 299110; CAA13172.1; -.
PIK; E69857; E68857.
Subtlist; BG13239; ohrR.
InterPro; IPR000335; HTH MarR.
Pfam; PF01047; MarR.
PRINTS; PR00598; HTHMARR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
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:: | :: | | | : | : | : | EMTKQYKPLLDKLNITYPQYLAL--LLLWEHETLITVKKWGGQLYLDSGTLTPMLKRMEQQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).

-!- MISCELLANDOUS: COMPONENT I CATALVZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERSE ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=26695 / ATCC 700392;
STRAIN=26695 / ATCC 700392;
MEDLINE=9734467; PubMed=9252185;
MEDLINE=9734467; PubMed=9252185;
Tomb J.-F., White O., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Venter J.C.;
                                                                                                                                                                                                                                                                                                                        Helicobarter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pylori.";
Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: Chorismate + L-glutamine = anthranilate
pyruvate + L-glutamate.
-!- PATHWAY: Tryptophan biosynthesis; first step.
-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006805; Anth synt I N.
InterPro; IPR005801; Anth—synth—chor.
InterPro; IPR005257; TrpE_prot.
Pfam; PF04715; Anth synt I N; 1.
Pfam; PF04715; Anth synt I N; 1.
Propon; PR00095; ANTSNTHAŠEI.
PRINTS; PR00095; ANTSNTHAŠEI.
ProDom; PR00079; Anth synth chor; 1.
TIGRFAMS; TIGR00565; TrpE proteon:
TIGRFAMS; TIGR00565; TrpE proteon:
Tryptophan blosynthesis; Lyase; Complete proteome.
SEQUENCE 500 AA; 56556 MW; B28485C36E1E635E CRC64;
                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB--2003 (Rel. 41, Last annotation update)
Anthranilate synthase component I (EC 4.1.3.27).
TRPE OR HF1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
15;
                                                                                                                                                                                             500 AA
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Pred. No.
                                                                                |:::||| :|||:|:||:
GLITRKRSEEDERSVLISLTE 102
                                                        76 KLLSKKRSLQDERTVIVYVTD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE000632; AAD08326.1; -. PIR, B64680, B64680, B64680, HSSP; P00897; 117Q. TIGR; HP1282; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%;
                                                                                                                                                                                           STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=210;
                                                                                                                                                                                           HELPY
                    24
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the ENBL Gutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLETE GENOME.
STRAIN=India-1967 / Isolate Ind3;
STRAIN=India-1967 / Isolate Ind3;
MEDLINE-93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
"Genes of variala and vaccinia viruses necessary to overcome the host protective mechanisms.";
FEBS Lett. 319:80-83(1991).
                                     14 TFQVKKFFRD---TKKKFNLNYEEI-YILNHILRSESNEISSKEIAKCSEFKPYYLTKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome
 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                              70 OKLKDLKLLSK-----KRSLQDERTVIVYVTDTQKANIQKLISELEEYIK 114
                                                                                                                                 196 QELQDLKELAKSIKSDFVPKKSKQ-SREVSANCSDSE---FEKRVLSLQEEIK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Potential virulence determinants in terminal regions of variola smallpox virus genome."; Nature 366:748-751(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIM=India-1967 / Isolate Ind3;
MEDLINE=93190624; PubMed=8383392;
Shchalkunov S.N., Blinov V.M., Totmenin A.V., Marennikova S.S.,
Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytorov V.V.,
Gashikov P.V., Belanov B.F., Belavin P.A., Resenchuk S.M.,
Andzhaparidze O.G., Sandakhohiev L.S.;
"Nucleotide sequence analysis of variola virus HindIII M, L, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [RNA](N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bangladesh-1975;
MEDLINE=84080747; PubMed=8264798;
Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
DNA-directed RNA polymerase 147 kDa polypeptide (EC 2.7.7.6)
RPO147 OR LGR OR UGR.
 Indels
39;
 24; Mismatches
                                                                                                                                                                                                                                            PRT; 1286 AA
                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X67119; CAA47582.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S55844; AAB24679.1; -. X69198; CAA49024.1; -. L22579; AAA60831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Res. 27:25-35(1993).
 32; Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=10255;
                                                                                                                                                                                                                                                                                                                                                                          Variola virus.
                                                                                                                                                                                                                                                                                                                                                                                                             Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter C.J.;
                                                                                                                                                                                                                                            VARV
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Query Match
Best Local Similarity 30.8%; Pred. No. 42;
Matches 33; Conservative 16; Mismatches 20; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ------OKLISELEEY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 CWNSECMQPYQKISFSKKKVCFVNKLDDINVPNSLIYQKLISIHEKF 176
                              InterPro; IPR000722; RNA_pol_A.
InterPro; IPR007081; RNA_pol_Rpbl_4.
InterPro; IPR007081; RNA_pol_Rpbl_4.
InterPro; IPR007081; RNA_pol_Rpbl_5.
InterPro; IPR006592; RNA_pol_Rpbl_5.
InterPro; IPR006592; RNA_pol_Rpbl_5.
IPR04983; RNA_pol_Rpbl_7; 1.
Pfam; PP04983; RNA_pol_Rpbl_7; 1.
Pfam; PP04989; RNA_pol_Rpbl_7; 1.
Pfam; PP04989; RNA_pol_Rpbl_7; 1.
Pfam; PP04989; RNA_pol_Rpbl_7; 1.
IPR06653; RNA_pol_Rpbl_5; 1.
IPR06653; RNA_pol_Rpbl_5; 1.
IPR06663; RNA_pol_Rpbl_5; 1.
ITR06663; RNA_pol_Rpbl_5; 1.
ITR06663; RNA_pol_Rpbl_6; 1.
                                                                                                                                                                                                                                        Early protein.
SEQUENCE 1286 AA; 146782 MW; EE9965ACBIDFA93B CRC64;
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Search completed: November 17, 2003, 12:43:37 Job time : 18 secs

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November 17, 2003, 12:24:25; Search time 52 Seconds (without alignments) 570.693 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELEEYIKN 115
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, GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9f0rl staphylococ	Q8cnc4 staphylococ	Q53600 staphylococ	Q53777 staphylococ	085233 staphylococ	Q99ta4 staphylococ	Q9ezk4 staphylococ	Q99rd5 staphylococ	Q8cnu6 staphylococ	Q9rfj6 staphylococ	Q9kwj2 staphylococ	Q8i3p4 plasmodium	Q96xy0 sulfolobus	099s05 staphylococ	Q8pgpl xanthomonas	OBores stanbylogo
ID	Q9F0R1	O8CNC4	053600	053777	085233	Q99TA4	Q9EZK4	Q99RD5	OBCINDE	OPRFJ6	Q9KWJ2	Q813P4	OAX36O	508660	Q8PQP1	OBCRES
	16	16	16	N	16	16	7	16	16	N	16	ın	17	16	16	16
% Query Match Length DB	115	114	124	113	124	153	247	247	66	166	250	1777	131	116	153	242
% Query Match	100.0	84.7	25.8	25.4	24.9	21.4	21.4	21.4	20.9	20.9	20.0	18.4	18.0	17.7	17.6	17.3
Score	574	486	148	146	143	123	123	123	120	120	115	105.5	103.5	101.5	101	66
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093r11 xanthomonas	Q8xlt0 clostridium							~		ın		Q8xjp0 clostridium	Ф	. Q8pds2 xanthomonas	Q8i3z6 plasmodium		O50574 bacillus ps				Q8ifm4 plasmodium	Q8mwp2 plasmodium	Q8mwpl plasmodium	Ω	Q8crf1 staphylococ		_	Q54123 staphylococ
Q93R11	Q8XLT0	Q8Y8B9	Q8CQ27	Q978Z3	Q92CI3	Q9CDU5	Q99VT5	QSEYB8	Q99RX6	Q8NV85	Q8I386	Q8XJP0	Q814T0	Q8PDS2	Q813Z6	P70734	050574	092001	Q8D349	051465	Q8IFM4	Q8MWP2	QSMWP1	Q8MWH2	Q8CRF1	Q92D32	Q8R6A0	054123
~	16	16	16	17	16	16	16	16	16		Ŋ	16	ഗ	16	ഹ	7	~	16	16	16	ហ	Ŋ	ŵ	ß	16	16	16	7
153	143	141	147	154	150	145	147	148	247	247	434	1185	959	153	513	145	148	157	628	2166	1697	1711	1713	1716	116	141	921	967
17.1	16.7		16.5			16.3		16.1	16.0		•		•		15.9	•	15.8	15.7	15.7		15.5	٠	•	15.5	15.4	15.4	15.4	15.4
	96	4.	94.5	4.		93.5	93.5	92.5	92	. 65	95	92	91.5	91	91	90.5	90.5	90	06	06	89	89	89	89	88.5	88.5	88.5	88.5
17	18	19	20		22			25				29	30	31	32	33	34	35	36	37	38	39	40	41	42		44	45

## ALIGNMENTS

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                                                                                                                                                                                                MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
Zhang Y., Far S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AR016750, AA005S09.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation update)
Staphylococcal accessory regulator variant (Staphylococcal accessory
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Baba T., Takeuchi F., Kurcda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Magai Y., Iwama N., Asano K., Naimi T., Kurcda H., Cui L.,
Yamamoto K., Hiramatuu K.;
"Genome and virulence determinants of high virulence community-
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0
                                                                                                                                                     100.0%; Score 574; DB 16; Length 115; 100.0%; Pred. No. 1.5e-36; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 114;
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                                                                                                                                115 AA; 13669 MW; D2CE40E2DB234DBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
SEQUENCE 114 AA; 13590 MW; A401B6F9FE6BBCAB CRC64;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 486; DB 16;
Pred. No. 6.9e-30;
8; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                      114 AA
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SARA OR SAVO616 OR SA0573 OR MW0580.
Staphylococcus aureus,
                                                                                                                                                                                                                                                                                                                      PRT;
                                                     acquired MRSA.";
Lancet 359:1819:1827(2002).
EMBL; APC207701; AAG35715:1; -.
EMBL; APC03136; BAB58457.1; -.
EMBL; APC03136; BAB943387.1; -.
EMBL; APC04829; BAB96078.1; -.
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                                                                                                                                                               Best Local Similarity 100. Matches 115; Conservative
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es 96; Conservative
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SEQUENCE 115 AA;
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SE1868.
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Q53600;
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MEDLINE-92335318; PubMed=1321441;
Cheung A.L., Koomey J.M., Butler C.A., Projan S.J., Fischetti V.A.;
"Regulation of exprotrein expression in Staphylococcus aureus by a
locus (aar) distinct from agr.";
Proc. Natl. Acad. Sci. U.S.A. 89:6462-6466(1992).
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SEQUENCE FROM N.A.
SEQUENCE S. aureus; STRAIN=WW2;
MEDLINE=220407117; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Tamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA.";
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                                                                                                                                                                                                                                                       SPECIES-S.aureus;
Shawcross S.G., Edwards-Jones V., Dawson M.M., Foster H.A.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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Staphylococcus aureus (strain MuSO / ATCC 700699), Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2).
Bacteria; Firmicuces; Bacillales; Staphylococcus.
NCBI_TaxID=1280, 158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-S.aureus; STRAIN=RN450;
MEDLINE-94292439; PubMed-8021198;
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SPECIES=S.aureus; STRAIN=RN450;
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SEQUENCE 124 AA;
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14731 MW; 4D1D10E47D574266 CRC64;

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124 AA;
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STRAIN=ATCC 12228;
Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fluckiger U., Wolz C., Cheung A.L.; "Characterization of a sar homolog of Staphylococcus epidermidis."; Infect. Immun. 0:0-0(1998).
KQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRI 115
                                                                                                                                                                                                                                                                                Cheung A.L., Projan S.J.;
"Cloning and sequencing of sark of Staphylococcus aureus, a gene required for the expression of agr.";
Bacteriol. 176:41649.
EMBL: U46541; AAB05396.1; -.
SEQUENCE 113 AA; 13469 MW; 6A6D53F34E010AFB CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2003 (TrEMBLrel. 23, Last annotation update)
Staphylococcal accessory regulator A homolog.
SARA OR SE0390.
                                                                                   Last sequence update)
Last annotation update)
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                            Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales; Staphylococcus.
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STRAIN=RN6390;
MEDLINE=94292439; PubMed=8021198;
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(TrEMBLrel. 01, I
(TrEMBLrel. 19, I
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Best Local Similarity 29.7v
Best Local 33; Conservative
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01-NOV-1996 (
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                                                                                                                                                3 ISKINDCFELLAMVTYADRLKGIIKKEFSISFEEFAVLTYISENKEESYYLKDIINHLNY
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                                                             Gaps
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Tamamato K., Hiramatsu K.;
"Genome and virilence determinants of high virulence community-acquired MRSA.";
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Last annotation update)
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ROT OR SAV1764 OR SA1583 OR MW1705.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain M15), and
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
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24.9%; Score 143; DB 16; 29.2%; Pred. No. 0.00076; tive 25; Mismatches 55;
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EMBL; AP003363; BAB57926.1; -.
EMBL; AP003135; BAB42851.1; -.
CMBL; AP004028; BAB95570.1; -.
COMDICTE PLOCHOME.
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Query Match
Best Local Similarity 29.24
Matches 33; Conservative
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SEQUENCE FROM N.A.
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Q8CNU6;
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Q9RFJ6
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Q8CNU6
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MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
MINOREMAN, OHGAT, Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutami-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattorii M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
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                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Milligan-Monroe K., Proctor R.A.; Milligan-Monara P.J., Milligan-Acterization of rlp, an Activator of the "The Isolation and Characterization of rlp, an Activator of the Staphylococcus aureus Virulence Factor Regulator Pathway Encoded by
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Bapai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
SarH2 protein (Staphylococcal accessory regulator A homolog).
SARH2 OR SAV2499 OR SA2287 OR MW2418
SLAPHYLOCOCCUS aureus (strain MM50 / ATC 700699),
Staphylococcus aureus (strain M315), and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; Score 123; DB 2; Length 247; 27.8%; Pred. No. 0.048; ive 26; Mismatches 52; Indels
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EMBL; AF288788; AAG45334.2; --
SEQUENCE 247 AA; 29792 MW; D078366866F60B2B CRC64;
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                  Staphylococcus aureus.
Bacceria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879, 158879, 196620;
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Lancet 359:1819-1827(2002).
EMBL; AP003365; BAB58661.1; -.
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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Analy Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin S.
Chang Y., Nen Y.,
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Complete proteons.
SEQUENCE 99 AA: 11800 WW; S8BDG8BC9BF837AE CRC64;
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                                                                                                                    21.4%; Score 123; DB 16; Length 2 27.8%; Pred. No. 0.048; ative 26; Mismatches 52; Indels
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Last sequence update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
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NCBI_TaxID=1280;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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Plasmodium falciparum (isolate 3D7)
   EMBL, AB035454; BAB03341.1;
EMBL, AP001129; BAB41327.1;
EMBL, AB050858; BAB69826.1;
EMBL, AP001358; BAB56274.1;
EMBL, AP004822; BAB53550.1;
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EMBL; AL929353; CAD51583.1;
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Matches 27; Conservative
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SEQUENCE 1777 AA;
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Biochem. Biophys. Res. Commun. 269:485-490(2000).
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101-CCT-2000 (TrEMBLrel. 15, Last sequence update)
101-CCT-2000 (TrEMBLrel. 15, Last sequence update)
101-CCT-2000 (TrEMBLrel. 15, Last sequence update)
1101-CCT-2000 (TrEMBLrel. 12, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 12, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 12, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 2, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 2, Last annotation update)
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1110-CCT-2000 (TrEMBLrel. 2, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 1, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 1, Last annotation update)
1110-CCT-2000 (TrEMBLrel. 1, Last annotation update)
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1110-CCT-2000 (TrEMBLrel. 1, Last annotation updat
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamanoto K., Hiramatu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                             14;
                                                                                                                                 Length 166;
                                                                                                                           20.9%; Score 120; DB 2; Length 16
28.0%; Pred. No. 0.055;
ive 26; Mismatches 45; Indels
J. Bacteriol. 182:3197-3203(2000).
EMBL; AF189239; AAF22306.1; -.
SEQUENCE 166 AA; 19431 MW; 251AE45481E5699D CRC64;
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                                                                                                                                                     Local Similarity 28.0% les 33, Conservative
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acquired MRSA.
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MEDLINE=2225708; PubMed=12368867;
Mingall K., Berman S., Atkin R., Baker S., Barron A., Brooks K.,
Mingall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherwach I., Chillingworth C.,
Crolin A., Davise B., Davis P., Dear P., Dearden F., Doggett U.,
Crolin A., Davises R., Goodhead I., Gabil H., Hanlin N., Hance Z.,
Raper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
Humphray S., Jagels K., James K.D., Johnson D., Lennard N.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price-C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares S., Stevens K.,
Sulston J. E., Craig A., Newbold C., Barrell B.G.,
Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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                                                                                                                                  Gaps
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Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                  DB 16; Length 250;
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250 AA; 29890 MW; 4680D50FE86DDC19 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                     55;
                                                           20.0%; Score 115; DB 1
25.0%; Pred. No. 0.19;
:ive 26; Mismatches
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Lancet 357:1225-1240(2001)
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                                                                                                                                        STRAIN=MW2
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Q8PQP1;
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MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ico T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawarabayssi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanawa T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
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                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-JUN 2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SAV2267 (Hypothetical protein MW2185).
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain Mu2), and
Staphylococcus aureus (strain Mu2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TAXID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Cenarchaeon, Sulfolobus tokodaii strain?";

DNA Res. 8:123-140(2001).

EMBL; AP000969; BAB67497.1; -.

InterPro.; IPR000835; HTH MarR.

PRINTS; PR00598; HTHMARR.

PRINTS; PR00598; HTHMARR.

SNART; SM0047; HTHMARR.

Hypothetical protein; Complete proteome.

SEQUENCE 131 AA; 15129 MW; E0A0AB5A3521EG3B CRC64;
                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein ST2388.
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                                                                                            PRELIMINARY;
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STRAIN=JCM 10545 / 7;
PubMed=11572479;
                                                                                                                                                                                                                                                           Sulfolobus tokodaii
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AC 099805
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RN (1)

SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REALNIB-206 / ATCZ 13902 / XV 101;

RX SIVAR N.D. (A FERRO J.A.) Reinach F.C., Farah C.S., Furlan L.R.,

RA Gaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bartolini M.C., Camargo L.B.A.,

RA Alves L.M.C., do Amaral A.M., Dartolini M.C., Camargo L.B.A.,

RA Alves L.M.C., Go Amaral A.M., Dartolini M.C., Camargo L.B.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Alves L.M.C., Go Maral D.B., Cursino-Santos J.R., El-Dorry H.,

RA Extayama A.M., Rishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Locali B.C., Machado M.A., Machara A.M. B.N., Martinez-Rossi.N.M.,

Martins E.C., Machado M.A., Manch R.M., Martinez-Rossi.N.M.,

Mortins E.C., Machado M.A., Okura V.K., Oliveira M.C., Oliveira M.C., Oliveira M.R.,

Mortins L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

"Thomparison Of the genomes of two Xanthomonas pathogens with differing
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                                                                                                                                                                                                                                                MEDLINE=22040717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; "Genome and virilence determinants of high virulence community-acquired MRSA.";
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Mhole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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EMBL; AP003364; BAB58429.1; -.

EMBL; AP004829; BAB64359.1; -.

EMBL; AP04829; BAB96050.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 116 AA; 13986 NW; CS7ACED821E33EF9 CRC64;
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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29.3%; Pred. No. 1;
vative 23; Mismatches
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Nature 417:459-463(2002).
EMBL; AE011663; AAV35173.1; -.
Interpro; IPR000835; HTH Marr.
Pfam; PF01047; Marr; 1.
PRINTS; PR00598; HTHMARR.
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SQ SEQUENCE 153 AA; 16888 MW; 58C5D2C55B3C71AA CRC64;
Query Match
Best Local Similarity 29.7%; Pred. No. 1.4;
Matches 27; Conservative 22; Mismatches 40; Indels 2; Gaps 1;
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<sup>70</sup> QKLKDLKLLSKKRSLQDERTVIVYVTDTQKA 100
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83 KRLQAAGLVSRTRAANDERQVIIALTETGRA 113

Search completed: November 17, 2003, 12:44:37
Job time: 56 secs

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Title: Perfect score:

Sednence:

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OM protein

Run on:

Scoring table:

Searched:

Database :

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APPLICANT: Trustees of Dartmouth College
TITLE OF INVENTION: Compositions and Methods for affecting virulence determinants in
TITLE OF INVENTION: Dacteria
FILE REPERBNCE: 11312-006-228
CURRENT APPLICATION NUMBER: PCT/US02/00877
CURRENT APPLICATION NUMBER: E0/261,233
PRIOR PILING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 35
SEQ ID NOS: 35
SEQ ID NOS: 35
SEQ ID NO 2
LENGTH: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Appl
Sequence 28, Appl
Sequence 6537, Ap
Sequence 6537, Ap
Sequence 6537, Ap
Sequence 5857, Ap
Sequence 5857, Ap
Sequence 6519, Ap
Sequence 6519, Ap
                                                                                                                                                                                                                                Sequence 35, Appl
Sequence 37, Appl
Sequence 3, Appli
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Sequence 9, Appli
Sequence 5183, Ap
Sequence 5183, Ap
Sequence 5181, Ap
Sequence 7381, Ap
Sequence 7381, Ap
Sequence 514, Ap
Sequence 614, Ap
Sequence 614, Ap
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                                                                                             Sequence 6523, Ap
Sequence 6487, Ap
Sequence 4993, Ap
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
                        Sequence 2, Appli
Sequence 4882, Ap
Sequence 6523, Ap
         Seguence
6 US-10-043-539-2
0 US-08-359A-2
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0 US-08-353A-2
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PCT-C802-00877-2
Sequence 2, Application PC/TUS0200877
GENERAL INFORMATION:
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    Sequence 2, Appli
                                                                                                                                                         November 17, 2003, 12:43:21; Search time 159 Seconds (without alignments) 658.117 Million cell updates/sec
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574
1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELBEYIKN 115
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2: (cg12 6) prodata/2/paa/USO6 COMB.ppp:*

5: (cg12 6) prodata/2/paa/USO7 COMB.ppp:*

5: (cg12 6) prodata/2/paa/USO3 1 COMB.ppp:*

6: (cg12 6) prodata/2/paa/USO3 1 COMB.ppp:*

7: (cg12 6) prodata/2/paa/USO3 2 COMB.ppp:*

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9: (cg12 6) prodata/2/paa/USO3 4 COMB.ppp:*

10: (cg12 6) prodata/2/paa/USO3 6 COMB.ppp:*

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                           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                 protein search, using
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Maximum DB seq length: 2000000000
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Match Length DB
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100.0

574 Score

Result No.

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1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYBEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                                                                                                                                                                                1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIXILNHILRSESNEISSKEIAKCSEF 60
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                                                                                                                                                                                                                                                                                                                                                                                   61 KPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN 115
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                                                                                                                               Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4882, Application US/08827356
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Hare
APPLICANT: Roberta S. Shaw
ITLLE OF INVENTION: COMPOSITIONS AND METHODS
ITLLE OF INVENTION: COMPOSITIONS AND METHODS
OWNERSPROMENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
                                                                                                                        Query Match 100.0%; Score 574; DB 26; Best Local Similarity 100.0%; Pred. No. 3.6e-49; Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match-
100.0%; Score 574; DB 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schering-Plough Corporation 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PERCENTING
SOFTWARE: PARCENTIN
CURRENT APPLICATION NUMBER: US/08/827,356
FILING DATE: 01-APR-1997
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/014,477
FILING DATE: 01-APR-1996
APPLICATION NUMBER: 60/016,743
FILING DATE: 14-UN-1996
APPLICATION NUMBER: 60/020,016
FILING DATE: 14-UN-1996
INFORMATION FOR SEQ ID NO: 4882:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN
                              ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Staphylococcus
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LOCATION: 1...129
US-08-827-356-4882
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GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose
APPLICANT: Manna, Adar
TITLE OF INVENTION: BACTERIA
TITLE OF INVENTION: BACTERIA
FILE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539
CURRENT APPLICATION NUMBER: US/202-01-11
FILE REPERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/202-01-11
FRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR PLILING DATE: 2001-01-12
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Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 2, Application US/10043539A

Sequence 3, Application Ambrose

APPLICANT: Cheung, Ambrose

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Manna, Adar

APPLICANT: Composition and METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN

FILE REFERENCE: DC-0199

CURRENT FILING DATE: 2000-01-11

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 35

SEQ ID NOS: 35

LENGTH: 115
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                                                                                                                                                                          1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF 60
                                                                                                                                  MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                                                                                                                                                                                                                                            KPYYLTKALQKLKOLKLLSKKRSLQDERTVIVYYTDTQKANIQKLISELEEYIKN 115
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      Length 115;
                                                                  0; Indels
Query Match 100.0%; Score 574; DB 1; Best Local Similarity 100.0%; Pred. No. 3.6e-49; Matches 115; Conservative 0; Mismatches. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539-2
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APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-09A
CURRENT APPLICATION NUMBER: US/09/450,969
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 7544
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: George H. Shimer,Jr.
APPLICANT: George H. Shimer,Jr.
APPLICANT: George H. Shimer,Jr.
APPLICANT: Roberte S. Hare
APPLICANT: Roberte S. Hare
APPLICANT: Roberte S. Hare
APPLICANT: Raren J. Shaw
TITLE OF INVENTION: Raphylococcus aureus Related Compositions and Methods
FILE REFRENCE: 1034/1C963US2
CURRENT APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR PELING DATE: 1999-03-11
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PRIOR PELING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR PELING DATE: 1999-03-11
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              1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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                                                                                                                                                                                          Gaps
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100.0%; Score 574; DB 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-49;
Matches 115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6487, Application US/09450969 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   S-09-950-084-6523
Sequence 6523, Application US/09950084
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-6523
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APPLICANT: George H. Shimer.Ur.
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APPLICANT: George H. Shimer.Ur.
APPLICANT: George H. Shimer.Ur.
APPLICANT: George H. Shimer.Ur.
APPLICANT: George H. Shimer.
APPLICANT: Rater. J. Shabylococcus aureus Related Compositions and Wethods
ITILE REPRESENCE: 1094/1265131
CURRENT APPLICANT: WINDSR: 10169/136,115
PRICE APPLICATION WINDSR: 1029/266,557
PRICE APPLICATION WINDSR: 1059/266,556
PRICE APPLICATION WINDSR: 1059/20-1109/266,556
PRICE APPLICATION WINDSR: 1059/20-1109/266,556
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Pred. No. 4.2e-49;
; Mismatches 0;
                                                                                                                                                                                                     Sequence 6523, Application US/09611529
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Best Local Similarity 100.
Matches 115; Conservative
                                                                                                                                                                        US-09-611-529-6523
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ORGANISM:
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Gaps

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Sequence 26, Application US/10043539
GENERAL INFORMATION:
APPLICANT: Chenng, Ambrose
APPLICANT: Chenng, Ambrose
APPLICANT: Chenng, Ambrose
APPLICANT: Zhang, Adar
APPLICANT: Zhang, Gongyi
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN
ITLE OF INVENTION: DATERIA
FILE REFERENCE: DC-0199
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/261,507
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-05-08
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                          NAME/KEY: SITE

LOCATION: 2,4,10,15,16,17,19,20,24,25,31,38,44,45,47,51,52,58,59,61,73,77,78,86,

LOCATION: 87,95,97,99,102, 106,110,114,117,118,120

CTHER INFORMATION: Xaa = any amino acid

PCT-US02-00877-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MXKINDIXDLLNXXXYXXKKFKXXIKKEFXLSFBEFXILTYIXXQXENBXXLKDIIXXLXY
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                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Consensus
                                                                                                                                                                                                                                                                                                                                                       ch 39.0%; Score 224; DB 1; Length 120; 1 Similarity 43.9%; Pred. No. 4.2e-14; 50; Conservative 15; Mismatches 49; Indels
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LOCATION: (19)...(20
LOCATION: (19)...(20
FEATURE: INFORMATION: "X" is defined as any amino acid residue.
PEATURE:
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LOCATION: (2)._(2)
OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid
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OTHER INFORMATION: "X" is defined as any
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Consensus sequence.
PEATURE:
SEQ ID NO 26
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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NAME/KEY: MISC FEATURE
LOCATION: (15)..(17)
OTHER INFORMATION: "X"
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NAME/KEY: MISC_FEATURE
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLEMBLIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-101
CURRENT APPLICATION NUMBER: US/10/092,411A
CURRENT APPLICATION NUMBER: US 09/134,001
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OS 5676
SEQ ID NOS: 5676
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                                                                                                                                                                                                                                                                              1 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEF
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84.2%; Pred. No. 2.7e-40;
tive 8; Mismatches 10;
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Best Local Similarity 84.2%;
Matches 96; Conservative
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Best Local Similarity 84.2
Matches, 96; Conservative
                                                       TYPE: PRT

ORGANISM: S.epidermidis

US-09-450-969-6487
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US-10-092-411A-4993
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PCT-US02-00877-26
     SEO ID NO 6487
LENGTH: 128
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NAME/KEY: MISC FEATURE LOCATION: (31)...(31) OTHER INFORMATION: "X" is defined as any amino acid residue. NAME/KEY: MISC\_FEATURE LOCATION: (114)..(114) LOCATION: (114)..(114) FEATURE: INFORMATION: "X" is defined as any amino acid residue. PEATURE: NAME/KEY: MISC\_FEATURE LOCATION: (24)... (25)
OTHER INFORMATION: "X" is defined as any amino acid residue NAME/KEY: MISC FEATURE LOCATION: (44)...(45) OTHER INFORMATION: "X" is defined as any amino acid residue ON: (47)...(47)
INFORMATION: "X" is defined as any amino acid residue. CON: (58)...(59)
INFORMATION: "X" is defined as any amino acid residue. OCATION: (73)...(73)
"THER INFORMATION: "X" is defined as any amino acid residue. NAME/KEY: MISC FEATURE LOCATION: (106). (106). OTHER INFORMATION: "X" is defined as any amino acid residue. LOCATION: (38)...(38) OTHER INFORMATION: "X" is defined as any amino acid residue ON: (61)..(61) INFORMATION: "X" is defined as any amino acid residue TION: (77)]. (78) R INFORMATION: "X" is defined as any amino acid residue LOCATION: (95)...(95) DTHER INFORMATION: "X" is defined as any amino acid residue ION: (102)..(102) INFORMATION: "X" is defined as any amino acid residue CATION: (86)...(87)
IER INFORMATION: "X" is defined as any amino acid residue INFORMATION: "X" is defined as any amino acid residue .OCATION: (99)7.(99) OTHER INFORMATION: "X" is defined as any amino acid residue LOCATION: (110)..(110) OTHER INFORMATION: "X" is defined as any amino acid residue NAME/KEY: MISC FEATURE COCATION: (51)...(52) NAME/KEY: MISC\_FEATURE NAME/KEY: MISC\_FEATURE JAME/KEY: MISC FEATURE JOCATION: (58)..(59) NAME/KEY: MISC\_FEATURE JAME/KEY: MISC FEATURE NAME/KEY: MISC\_FEATURE NAME/KEY: MISC\_FEATURE AME/KEY: MISC\_FEATURE NAME/KEY: MISC FEATURE NAME/KEY: MISC\_FEATURE NAME/KEY: MISC FEATURE LOCATION: (110)..(110) NAME/KEY: MISC\_FEATURE NAME/KEY: MISC FEATURE COCATION: (102)

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APPLICANT: Cheung, Ambrose

APPLICANT: Manna, Adar

APPLICANT: Cheung, Ambrose

APPLICANT: Cheung, Gongyi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN

FILE REFERENCE: DC-0199

CURRENT APPLICATION NUMBER: US/10/043,539A

CURRENT FILING DATE: 2000-01-11

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/261,607

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/289,601

PRIOR APPLICATION NUMBER: US 60/289,601

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CCATION: (117)...(118)

OTHER INFORMATION: "X" is defined as any amino acid residue.

FEATURE: NAME/KEY: MISC_PEATURE

LOCATION: (120)...(120)

OTHER INFORMATION: "X" is defined as any amino acid residue.
US-10-043-539-26
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LOCATION: (2)...(2)
UNIER INFORMATION: "X" is defined as any amino acid residue.
FEATURE: NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue.
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OTHER INFORMATION: "X" is defined as any amino acid residue
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OTHER INFORMATION: "X" is defined as any amino acid residue
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NAME/KEY: MISC FEATURE
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NAME/KEY: MISC_FEATURE
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PCT-USO2-00877-35

Sequence 35, Application PC/TUSO200877

Sequence 35, Application PC/TUSO200877

Sequence 35, Application PC/TUSO200877

SEQUENCE INFORMATION:

APPLICANT Trustees of Dartmouth College

TITLE OF INVENTION: Compositions and Methods for affecting virulence determinants in TITLE OF INVENTION: Dacteria

FILE REFERENCE: 11312-006-228

CURRENT APPLICATION NUMBER: PCT/USO2/00877

CURRENT APPLICATION NUMBER: 60/261,233

PRIOR FILING DATE: 2001-01-12

PRIOR PELICATION NUMBER: 60/261,607

PRIOR PELICATION NUMBER: 60/269,601

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 60/289,601

PRIOR FILING DATE: 2001-01-05-08

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Version 3.2
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US-10-043-539A-35
Sequence 35, Application US/10043539A
Sequence 35, Application US/10043539A
Sequence 35, Application US/10043539A
SPECIANT: Cheung, Ambrose
APPLICANT: Manna, Adar
APPLICANT: Cheung, Gongyi
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR AFFECTING VIRULENCE DETERMINANTS IN FILE REFERENCE: DC-0199
CURRENT APPLICATION NUMBER: US/10/043,539A
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/261,607
PRIOR PAPLICATION NUMBER: US 60/261,607
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-14
SPIOR FILING DATE: 2001-03-15
SPIOR FILING DATE: 2001-03-15
SPIOR FILING DATE: 2001-03-15
SPIOR FILING DATE: 2001-03-15
SPIOR FILING DATE: 2001-03-15
SPIOR FILING DATE: 2001-03-15
SEQ ID NO 35
LENGTH: 120
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                                                 39.0%; Score 224; DB 26; Length 120; 43.9%; Pred. No. 4.2e-14; tive 15; Mismatches 49; Indels
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                                                    Query Match
Best Local Similarity 43.9%
Matches 50; Conservative
US-10-043-539A-26
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LENGTH: 120
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1 MSKINDINDLVNATFÇVKKFFRDTKKKFNLNYEE1Y1LNHILRSESNEISSKEIAKCSEF 60
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                                                                                                             Length 124;
                                                                                                                                                              52; Indels
                                                                                                       Query Match

25.8%; Score 148; DB 20;
Best Local Similarity 30.1%; Pred. No. 1.8e-06;
Matches 34; Conservative 27; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: November 17, 2003, 12:48:22
he : 161 secs
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-612-549A-1
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; Sequence 1, Application US/09612549A
; GENERAL INFORMATION:
APPLICANT: HURLBURT, Barry
APPLICANT: SMELTZER, Mark
APPLICANT: SMELTZER, Mark
APPLICANT: RECHTIN, Tammy
TITLE OF INVENTION: EXPRESSION OF STAPHYLOCOCCUS SARA PROTEIN FUNCTION INVOLVED IN TH
TITLE OF INVENTION: STAPHYLOCOCCAL UNFECTIONS
TITLE OF INVENTION: STAPHYLOCOCCAL INFECTIONS
TOURRENT FILING DATE: 1090-07-07
PRIOR PILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTH VERSION 3.0
SEQ ID NO 1
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application PC/TUS0200877

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for affecting virulence determinants in TITLE OF INVENTION: Dacteria
FILE REFERENCE: 11312-06-228
CURRENT APPLICATION NUMBER: PCT/US02/00877
CURRENT PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261,233
PRIOR PILING DATE: 2001-01-12
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-03-04
NUMBER: 60/269,601
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
FEATURE OF THE PERMINE PATENTIAL NUMBER: PATENTIAL NUMBER: PATENTIAL NUMBER: PATENTIAL NUMBER: 60/269,601
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                 52; Indels
                                                                                                       Query Match

25.8%; Score 148; DB 26;
Best Local Similarity 30.1%; Pred. No. 1.7e-06;
Matches 34; Conservative 27; Mismatches 52;
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ORGANISM: Staphylococcus aureus
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-043-539A-35
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Matches 34; Conservative
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PCT-US02-00877-3
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Sequence 2, Appli
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Sequence 20147, A
Sequence 25, Appl
Sequence 25, Appl
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116, App
2207, App
35, Appl
35, Appl
1802, Appl
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111, App
1432, Ap
68716, A
2, Appli
25933, A
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82.045 Million cell updates/sec
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1 MSKINDINDLVNATFQVKKF......DTQKANIQKLISELEEYIKN 115
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'Ggn2_6/ptodata/2/paa/USOF_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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'Ggn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

'Ggn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*
         GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-10-425-114A-68716
US-10-332-089-2
US-10-679-063-25933
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US-10-679-063-18206

US-10-673-119-25

US-10-673-119-25

US-10-673-119-25

US-10-671-134-25

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                                                                                                              November 17, 2003, 12:43:40
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Maximum Match 100%
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No.
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27 75 13.1 746 6 US-10-425-114A-62635 Sequence 62635, A Squares 13.1 1230 7 US-60-479-073-342 Sequence 342, App 29 13.1 1230 7 US-60-479-073-342 Sequence 342, App 30 74 5 13.0 1014 5 US-00-479-073-340 Sequence 211, App 31 174.5 13.0 1373 6 US-10-473-040-719 Sequence 211, App 32 74 12.9 186 US-10-473-040-719 Sequence 719, App 32 17 12.9 236 5 US-10-976-976-976-9999 Sequence 25849, A 12.9 236 5 US-10-979-979-979-9999 Sequence 25849, A 2.5 12.8 4.99 6 US-10-296-115-801 Sequence 258945, A 2.5 12.8 4.99 6 US-10-296-115-801 Sequence 258945, A 2.7 12.7 732 6 US-10-679-063-25845 Sequence 258945, A 2.7 12.7 12.96 6 US-10-679-063-25483 Sequence 258945, A 2.7 12.6 5 US-10-205-2164-1 Sequence 25948, A 2.7 12.6 5 US-10-205-2164-1 Sequence 25946, A 2.7 12.6 5 US-10-679-063-25946 Sequence 25946, A 2.7 12.6 5 US-10-679-063-25946 Sequence 25946, A 2.7 12.6 5 US-10-679-063-25946 Sequence 25946, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25946, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25940, A 2.7 12.6 5 US-10-679-063-25940 Sequence 25941, A 2.7 12.6 5 US-10-679-063-25941 Sequence 25941, A 2.7 12.6 5 US-10-679-063-25941 Sequence 25941, A 2.7 12.6 5 US-10-679-063-25941 Sequence 25941, A 2.7 12.6 5 US-10-679-063-25941 Sequence 25941, A 2.7 12.6 5 US-10-679-063-25941 Sequence 25941, A 2.7 12.6 12.6 12.6 12.6 12.
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## ALIGNMENTS

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APPLICANT: Trustees of Dartmouth College
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN BA
TITLE REPERBNEE: DC-0.188.
CURRENT APPLICATION NUMBER: US 60/273,791
PRIOR PILING DATE: 2001-03-06
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-08-15
PRIOR PILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN NUMBER: US 60/329,140
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 134
TYPE: PRT
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| Sequence 2, Application US/10469477
| Sequence 2, Application US/10469477
| GENERAL INFORMATION:
| APPLICANT: Trustees of Dartmouth College
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING AUTOLYTIC PROCESSES IN |
| FILE REPERBENCE: DC-0188
| FULE REPERBENCE: DC-0188
| CURRENT APPLICATION NUMBER: US/10/469,477
| CURRENT FILING DATE: 2003-08-27
| PRIOR FILING DATE: 2001-03-06
| PRIOR PLILING DATE: 2001-08-15
| PRIOR PLILING DATE: 2001-08-15
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16.3%; Score 93.5; DB 6;
Best Local Similarity 28.4%; Pred. No. 8.8;
Matches 25; Conservative 25; Mismatches 35;
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US-10-469-477-4; Sequence 4, Application US/10469477; GENERAL INFORMATION:
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24.2%; Pred. .v..
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14.2%; Score 81.5; I
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches
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US-10-673-119-25
Sequence 25, Application US/10673119
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzieva, Olga
APPLICANT: Jeruzalmi, David
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US-10-673-119-25
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         Best Local Similarity
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US-10-673-120-25
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                              Matches
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                                                                                                                                                                                                                                                                                                                      10 LVNATFOVKKFFRD-TKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKA 68
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US-10-679-063-20147
US-10-679-063-20147
Sequence 20147, Application US/10679063
Sequence 20147, Application US/10679063
SIGNERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION TRANSGRIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15 (25054)B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 20147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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Sequence 18206, Application US/10679063
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
TILE REFERENCE: 38-15(52054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR PILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 19206
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                                                                                                                                                                                                                             16.3%; Score 93.5; DB 6; Length 147; llarity 28.4%; Pred. No. 9.3; Conservative 25; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 91; DB 6; Length 513; 28.0%; Pred. No. 29; tive 24; Mismatches 38; Indels
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       PRIOR APPLICATION NUMBER: US 60/329,140 PRIOR FILING DATE: 2001-10-12 NUMBER OF SEQ ID NOS: 4 SOFTWARE: Patentin version 3.1 SEQ ID NO 2
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                                                                                                                   LENGTH: 147

TYPE: PRT

ORGANISM: Staphylococcus aureus
US-10-469-477-2
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; ORGANISM: Rattus norvegicus
US-10-679-063-20147
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Matches 28; Conserv
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APPLICANT: Yurieva, Olga
APPLICANT: Yurieva, Olga
APPLICANT: Yurieva, Olga
APPLICANT: Jeruzalmi, David
APPLICANT: Jeruzalmi, David
APPLICANT: Burck, Irina
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TITLE OF INVENTION: USE THEREOF
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TITLE OF INVENTION: USE 199-2-6
FRICK APPLICATION NUMBER: US/09/716,964A
FRICK FLING DATE: 1990-01-21
FRICK APPLICATION NUMBER: 06/143,202
FRICK APPLICATION NUMBER: 06/143,202
FRICK APPLICATION NUMBER: 09/057,416
FRICK FILING DATE: 1997-04-08
FRICK APPLICATION NUMBER: 09/057,416
FRICK FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 25
LENGTH: 260
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                                                                                                         2 SKINDINDLVNATFQVKKFFRD-TKKKFNLNYEE-----IYILNHILRSESNEISSKEI 54
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51; Indels
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US-10-671-134-25

i Gequence 25, Application US/10671134

GENERAL INFORMATION:

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Alexander

APPLICANT: Vurbackov, Olga

APPLICANT: Wurback, Irina

APPLICANT: Bruck, Irina

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APPLICANT: Bruck, Irina

APPLICANT: Warryan, John

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FILE REFERENCE: 2022/1/134

CURRENT PAPLICATION NUMBER: US/09/716,964A

PRIOR FILING DATE: 1997-04-08

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47 -----NEISSKEIAKCSE--FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT 95
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Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37; Indels 4
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US-10-673-120-25
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APPLICANT: Yuzhakov, Alexander
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APPLICANT: Yuzhakov, Olga
APPLICANT: Bruck, Irina
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PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/143, 202
PRIOR APPLICATION NUMBER: 60/143, 202
PRIOR APPLICATION NUMBER: 60/143, 202
PRIOR APPLICATION NUMBER: 00/0823, 407
PRIOR PILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PATENTIN VOR: 2.1
SEQ ID NO 25
TEMPORE DATE: 20.0
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14.2%; Score 81.5; DB 6; Length 260;
22.8%; Pred. No. 70;
:ive 27; Mismatches 37; Indels 4
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14.2%; Score 81.5; DB 6; 1
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37;
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APPLICANT: O'Donnell, Michael E.
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/10673098 GENERAL INFORMATION:
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US-10-673-098-25
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DLSQGSLRDGLSLLDQ 222
                            Best Local Similarity 22.8
Matches 31; Conservative
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TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: 'Unonell, Michael E.
APPLICANT: 'Urahakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Olga
APPLICANT: Yuzhakov, Olga
APPLICANT: Wariyan, John
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: UNBER: US/09/716,964A
TITLE OF INVENTION UNBER: US/09/716,964A
CURRENT APPLICATION NUMBER: US/09/716,964A
CURRENT FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 09/057,416
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USC THEREOF
TITLE OF INVENTION: USC THEREOF
TITLE OF INVENTION WIMMER: US/09/716, 964A
PRICK APPLICATION NUMBER: 06/143, 202
PRICK APPLICATION NUMBER: 60/143, 202
PRICK APPLICATION NUMBER: 60/143, 202
PRICK PILING DATE: 1997-04-08
PRICK PILING DATE: 1997-04-08
PRICK PILING DATE: 1998-04-08
PRICK PILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 260;
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14.2%; Score 81.5; DB 6; Length 2.
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37; Indels
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; ORGANISM: Mycoplasma genitalium
US-10-670-844-25
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US-10-673-127-25
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 260
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US-10-670-844-25
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APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Alexander
APPLICANT: Yuzhakov, Olga
APPLICANT: Bruck, Itha
APPLICANT: Bruck, Itha
APPLICANT: Bruck, Itha
APPLICANT: Bruck, Itha
APPLICANT: Wutiyan, John
ITILE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE OF 10/90/10/671,403
CURRENT APPLICATION NUMBER: US/10/671,403
CURRENT FILING DATE: 2000-11-21
PRIOR PILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR PILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
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                                                          Gaps
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   DB 6; Length 260;
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14.2%; Score 81.5; DB 6; Length 26
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37; Indels
                                                       37; Indels
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14.2%; Score 81.5; DB 22.8%; Pred. No. 70; tive 27; Mismatches
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US-10-671-859-25
; Sequence 25, Application US/10671859
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/10671403 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Mycoplasma genitalium
US-10-671-403-25
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   Query Match
Best Local Similarity 22.84
Matches 31; Conservative
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DTOKANIOKLISELEE 111
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) ORGANISM: Borrelia burgdorferi
US-10-688-058-60
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244 KIKSVEYKKILEELD 258
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APPLICANT: Yurieva, Olga
APPLICANT: Jeruzalmi, David
APPLICANT: Jeruzalmi, David
APPLICANT: Bruck, Irina
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
ITILE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE THEREOF
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ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION: USE THEREOF
ITILE OF INVENTION NUMBER: US/10/671,859
CURRENT FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
PRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
COTTMARE: PARCENTION VUMBER: OS/057,416
NUMBER OF SEQ ID NOS: 212
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GENERAL INFORMATION:

APPLICANT: Vicheva, Olga
APPLICANT: Vicheva, Olga
APPLICANT: Vicheva, Olga
APPLICANT: Vicheva, Olga
APPLICANT: Vicheva, Olga
APPLICANT: Sequence Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice Sevice 
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14.2%; Score 81.5; DB 6;
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Mycoplasma genitalium
US-10-671-859-25
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ORGANISM: Mycoplasma genitalium
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Sequence 60, Application US/10688058

GENERAL INFORMATION:
APPLICANT: SYKES, KATHRYN F.
APPLICANT: SYKES, KATHRYN F.
APPLICANT: HALE, KATHRYNE S.
APPLICANT: HALE, KATHRYNE S.
APPLICANT: JOHNSTON, STEPHEN A.
ITILE OF INVENTION: MCHICALE AND COMPOSITIONS FOR VACCINATION COMPRISING
ITILE OF INVENTION: MCHICAL AND/OR POLYPEPTIDE SEQUENCES OF THE GENUS
TILLE OF INVENTION: BORRELIA
TILLE OF INVENTION: BORRELIA
CURRENT APPLICATION NUMBER: US/10/688,058
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 60.
                                                                                                                                                                                                                                                                                                                150 LFIFTTTEFNKIPLTILSRCQSFFFKKITSDLILERLND---IAKKEKIKIEKDALIKIA 206
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                                                                                                                                                                                                                                                              47 ------NEISSKEIAKCSE--FKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 ----SESNEI----SSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVT 95
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GENERAL INFORMATION:
GENERAL INFORMATION:
TUTLE OF INVENTION:
FILE REFERENCE: 70035-5241-RCT
CURRENT APPLICATION NUMBER: 2003-09-02
FILE REFERENCE: 2003-09-02
FILE REFERENCE: 2003-09-02
FILE REFERENCE: 2003-09-02
FILE REFERENCE: 2003-09-02
FILE REFERENCE: 2003-09-02
FILE OF INVENTION NUMBER: US 60/407,082
FILE OF FILE OF SEQ ID NOS: 560
SOFTWARE: Patentin version 3.2
LENGTH; 428
                                                                                                                                                                             |||| :|| :|| :|| 100 INDIRELVENVENHPFTF---KKK------VYILDEAHMLTIQSWGGLLKTLEESPPYV
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Length 260;
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13.9%; Score 80; DB 6; Length 112
Best Local Similarity 22.2%; Pred. No. 2.1e+02;
Matches 30; Conservative 27; Mismatches 50; Indels
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Query Match
14.2%; Score 81.5; DB 6; 1
Best Local Similarity 22.8%; Pred. No. 70;
Matches 31; Conservative 27; Mismatches 37;
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae PCT-US03-27401-259
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Ouery Match 13.9%; Score 79.5; DB 1; Length 428; Best Local Similarity 25.8%; Pred. No. 1.3e+02; Matches 24; Conservative 20; Mismatches 36; Indels 13; Gaps 3;

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Search completed: November 17, 2003, 12:49:36 Job time : 68 secs

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